

SEQUENCE LISTING

<110> Patience, Clive

<120> Gamma Herpes Virus DNA and Methods of Use

<130> 61750-379

<150> US/09/612,204

<151> 2000-07-07

<150> US/60/142,736

<151> 1999-07-08

<150> US/60/168,532

<151> 1999-12-02

<160> 55

<170> PatentIn version 3.0

<210> 1

<211> 585

<212> DNA

<213> artificial

<220>

<223> Fragment from Swine Gamma Herpesvirus DNA coding for glycoprotein B envelope protein

<400> 1

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aactgtattg	tggtagacca	aaccagtgtc	tcattacata	aaagtctcag	gcttctcagt	240
gcatcggatg	aaaagtgtct	ctctagacct	ccagtgacat	ttaagtttat	gaatgacagt	300
actattttaca	aagggcaact	aggagtcaat	aatgagattc	tcttaaccac	aacatacctt	360
gaaacatgtc	aggaaaacac	tgagtattac	tttcaggcaa	agacagacat	gtacattttac	420
aaaaactatg	agcattttgaa	gactgtgcct	ttatcttcga	tcaccacact	agatacattt	480
atagccctta	attttacact	attggagaat	gttgacttta	aagtcattga	actttatacc	540
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<210> 2

<211> 195

<212> PRT

<213> artificial

<220>

<223> Deduced amino acid sequence derived from the first open reading frame of the DNA of SEQ ID NO:

<400> 2

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<210> 5
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<212> DNA
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<220>

<223> PCR amplification primer for pGHV-gpB gene sequences

<400> 5

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17

<210> 6
<211> 19
<212> DNA
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<220>

<223> PCR amplification primer for pGHV-gpB gene sequences

<400> 6

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19

<210> 7
<211> 19
<212> DNA
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<220>

<223> PCR amplification primer for pGHV-gpB gene sequences

<220>

<221> misc_feature

<223> n=i

<400> 7

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19

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<223> PCR amplification primer for pGHV-gpB gene sequences

<400> 8

gtbatgwsha gvathtaygg

20

<210> 9
<211> 20
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<220>
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<400> 9
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<210> 10
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<220>
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<220>
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<210> 12
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<400> 12
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<210> 13
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 <220>
 <223> PCR amplification primer for Epstein-Barr Virus genome

 <400> 15
 agaactaccg tcaactgcct 20

 <210> 16
 <211> 18
 <212> DNA
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 <220>
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 <400> 16
 agaactaccg tcaactgc 18

 <210> 17
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 <400> 17
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<210> 18
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<210> 20
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 <400> 20
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<210> 21
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 <212> DNA
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 <220>
 <223> PCR amplification primer for Epstein-Barr Virus genome

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<210> 22
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<210> 23
<211> 2598
<212> DNA
<213> artificial

<220>
<223> cDNA for porcine gamma herpesvirus gpB gene

<400> 23
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tggctactctg aatcgccgct aacagggtcac tatggaacac acgattcaag ccatggtgaa 180
agaggaaaca acgaaaacag agattcagaa gagcaaaata aaaacattta tggatcgccct 240
tctacgtttc cttacagagt atgcagtgcc tccggagttg gagatgtctt tagatttcag 300
accgaccatg tgtgtcccga tgccagtgat atggtacaca gtgaggggat tctactaatt 360
tacaacagat acattattcc atttatgttt agagttagga aatatagaaa agttgttaca 420
acaagtactg tctacaatgg tattttattct gactctatta ccaaccaaca tactttctat 480
aaatcaatcg aaccttgagg gacagaaaag atggacacaa tatatcagtg ttttaattct 540
ttaagactaa acacagggtg aaatctgctt acttatgtag atagagatga tataaatatg 600
acagtgtttc tgcaacctgt tgacgggtgtg acgcccgatg tgaagaggta tggcagtcaa 660
ccagagctgt accttgaacc tggctgggtt tggggtagtt atagaagacg aactacagtg 720
aactgtgaac taatggacat gtttgcaaga tcaaactctc catttgattt ctttgttaca 780
gctacagggtg atacggtgga aatgtctcca ttttgagggtg gtgaagatga tcatgaaaat 840
aagatgcacg agaagccatg gtttggttagt gtgataaata actacaaggt ggtggactat 900
caaaacagag ggactgtacc ccttggaana acaaggatat ttctagatag ggaagagtat 960
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gcattttaca atggaatcca gacggagcat tcagggtcat atcattttgt agccaatgac 1080
atcacagcgt cattcacaac tagtaaagaa gacatgaaag agttcaatac gacatatcat 1140
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tacattttaca aaaactatga gcattttgaag actgtgcctt tatcttcgat caccacacta 1920
gatacattta tagcccttaa ttttacacta ttggagaatg ttgactttaa agtcattgaa 1980
ctttatacca gggacgagaa gaggttagt aatgtctttg acattgaaac aatgtttagg 2040
gaatataact actatgctca gaggttcagt ggcctcagaa aggatttgct ggatctaagc 2100
accaatagaa atcaaatgtg ggatgcattt ggtagtctta tggatgattt ggggtgctgtt 2160
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gcaccaatca gtgaagaaga gctggagaga attgtacttg ctatgcacat ccatcaacaa 2460
aattcacata tggaaacaaa aacaaggaag gatcccaaag acagcatatt aacaagggca 2520
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atgttaaaca ctttataa 2598

<210> 24
 <211> 865
 <212> PRT
 <213> artificial

<220>

<223> Deduced amino acid sequence of porcine gamma herpesvirus gpB gene

<400> 24

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Leu Tyr Gln Val Ala Leu Tyr Ser Leu Ser Ile Ala Glu Thr Gly Val
 20 25 30

Thr Ser Pro Pro Asn Thr Ala Thr Trp Ser Thr Glu Ser Pro Leu Thr
 35 40 45

Gly His Tyr Gly Thr His Asp Ser Ser His Gly Glu Arg Gly Asn Asn
 50 55 60

Glu Asn Arg Asp Ser Glu Glu Gln Asn Lys Asn Ile Tyr Gly Ser Pro
 65 70 75 80

Ser Thr Phe Pro Tyr Arg Val Cys Ser Ala Ser Gly Val Gly Asp Val
 85 90 95

Phe Arg Phe Gln Thr Asp His Val Cys Pro Asp Ala Ser Asp Met Val
 100 105 110

His Ser Glu Gly Ile Leu Leu Ile Tyr Lys Gln Asn Ile Ile Pro Phe
 115 120 125

Met Phe Arg Val Arg Lys Tyr Arg Lys Val Val Thr Thr Ser Thr Val
 130 135 140

Tyr Asn Gly Ile Tyr Ser Asp Ser Ile Thr Asn Gln His Thr Phe Tyr
 145 150 155 160

Lys Ser Ile Glu Pro Trp Glu Thr Glu Lys Met Asp Thr Ile Tyr Gln
 165 170 175

Cys Phe Asn Ser Leu Arg Leu Asn Thr Gly Gly Asn Leu Leu Thr Tyr
 180 185 190

Val Asp Arg Asp Asp Ile Asn Met Thr Val Phe Leu Gln Pro Val Asp
 195 200 205

Gly Val Thr Pro Asp Val Lys Arg Tyr Gly Ser Gln Pro Glu Leu Tyr
 210 215 220

Leu Glu Pro Gly Trp Phe Trp Gly Ser Tyr Arg Arg Arg Thr Thr Val
 225 230 235 240

Asn Cys Glu Leu Met Asp Met Phe Ala Arg Ser Asn Pro Pro Phe Asp
 245 250 255

Phe Phe Val Thr Ala Thr Gly Asp Thr Val Glu Met Ser Pro Phe Trp
 260 265 270
 Ser Gly Glu Asp Asp His Glu Asn Lys Met His Glu Lys Pro Trp Phe
 275 280 285
 Val Ser Val Ile Asn Asn Tyr Lys Val Val Asp Tyr Gln Asn Arg Gly
 290 295 300
 Thr Val Pro Leu Gly Lys Thr Arg Ile Phe Leu Asp Arg Glu Glu Tyr
 305 310 315 320
 Thr Leu Ser Trp Glu Lys His Leu Lys Asn Met Ser Tyr Cys Pro Leu
 325 330 335
 Thr Leu Trp Lys Ala Phe Tyr Asn Gly Ile Gln Thr Glu His Ser Gly
 340 345 350
 Ser Tyr His Phe Val Ala Asn Asp Ile Thr Ala Ser Phe Thr Thr Ser
 355 360 365
 Lys Glu Asp Met Lys Glu Phe Asn Thr Thr Tyr His Cys Leu Asn Glu
 370 375 380
 Glu Ile Lys Ala Glu Ile Glu Lys Lys Tyr Ala Lys Val Asn Ser Thr
 385 390 395 400
 His Ser Lys Tyr Gly Asp Leu Lys Tyr Phe Lys Thr Asp Gly Gly Leu
 405 410 415
 Tyr Leu Val Trp Gln Pro Leu Ile Gln Asn Arg Leu Leu Asp Ala Lys
 420 425 430
 Asn Lys Leu Asn Asn Glu Thr Tyr Ser Arg Arg Ser Arg Arg Gln Ala
 435 440 445
 Glu Ser Thr Thr Asp Pro Met Met Glu Met Thr Gly Asn Gly Ala Gly
 450 455 460
 Gly Glu Tyr Ser Ser Glu Asn Ser Ile Thr Val Ala Gln Val Gln Tyr
 465 470 475 480
 Ala Tyr Asp Asn Leu Arg Ile Arg Ile Asn Asn Ile Leu Glu Asp Leu
 485 490 495
 Ser Lys Ala Trp Cys Arg Glu Gln His Arg Ala Ala Leu Val Trp Asn
 500 505 510
 Glu Leu Ser Lys Ile Asn Pro Thr Ser Val Met Ser Met Ile Tyr Asn
 515 520 525
 Arg Pro Val Ser Ala Lys Arg Ile Gly Asp Val Ile Ser Val Ser Asn
 530 535 540
 Cys Ile Val Val Asp Gln Thr Ser Val Ser Leu His Lys Ser Leu Arg
 545 550 555 560

Leu	Leu	Ser	Ala	Ser	Asp	Glu	Lys	Cys	Phe	Ser	Arg	Pro	Pro	Val	Thr		
				565					570					575			
Phe	Lys	Phe	Met	Asn	Asp	Ser	Thr	Ile	Tyr	Lys	Gly	Gln	Leu	Gly	Val		
			580					585					590				
Asn	Asn	Glu	Ile	Leu	Leu	Thr	Thr	Thr	Tyr	Leu	Glu	Thr	Cys	Gln	Glu		
		595					600					605					
Asn	Thr	Glu	Tyr	Tyr	Phe	Gln	Ala	Lys	Thr	Asp	Met	Tyr	Ile	Tyr	Lys		
	610					615				620							
Asn	Tyr	Glu	His	Leu	Lys	Thr	Val	Pro	Leu	Ser	Ser	Ile	Thr	Thr	Leu		
625				630					635						640		
Asp	Thr	Phe	Ile	Ala	Leu	Asn	Phe	Thr	Leu	Leu	Glu	Asn	Val	Asp	Phe		
			645						650					655			
Lys	Val	Ile	Glu	Leu	Tyr	Thr	Arg	Asp	Glu	Lys	Arg	Leu	Ser	Asn	Val		
		660						665					670				
Phe	Asp	Ile	Glu	Thr	Met	Phe	Arg	Glu	Tyr	Asn	Tyr	Tyr	Ala	Gln	Arg		
	675						680					685					
Val	Ser	Gly	Leu	Arg	Lys	Asp	Leu	Leu	Asp	Leu	Ser	Thr	Asn	Arg	Asn		
	690					695					700						
Gln	Phe	Val	Asp	Ala	Phe	Gly	Ser	Leu	Met	Asp	Asp	Leu	Gly	Ala	Val		
705				710					715					720			
Gly	Gln	Thr	Val	Val	Asn	Ala	Val	Ser	Gly	Val	Ala	Thr	Leu	Phe	Ser		
			725						730				735				
Ser	Ile	Val	Thr	Gly	Phe	Ile	Asn	Phe	Ile	Lys	Asn	Pro	Phe	Gly	Gly		
	740						745						750				
Met	Leu	Met	Ile	Ile	Val	Val	Ile	Gly	Val	Leu	Phe	Ala	Ile	Tyr	Phe		
	755						760					765					
Leu	Thr	Lys	Lys	Thr	Lys	Ile	Tyr	Glu	Thr	Ala	Pro	Ile	Lys	Met	Ile		
	770					775					780						
Tyr	Pro	Glu	Ile	Asp	Lys	Leu	Lys	Glu	Arg	Glu	Gly	Lys	Ser	Glu	Ile		
785				790					795					800			
Ala	Pro	Ile	Ser	Glu	Glu	Glu	Leu	Glu	Arg	Ile	Val	Leu	Ala	Met	His		
			805						810					815			
Ile	His	Gln	Gln	Asn	Ser	His	Met	Glu	Thr	Lys	Thr	Arg	Lys	Asp	Pro		
		820						825					830				
Lys	Asp	Ser	Ile	Leu	Thr	Arg	Ala	Gln	Asn	Met	Leu	Arg	Lys	Arg	Ser		
	835					840						845					
Gly	Tyr	Ser	Asn	Leu	Lys	Asn	Ala	Glu	Ser	Val	Glu	Met	Leu	Asn	Thr		
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Leu
865

<210> 25
<211> 24
<212> DNA
<213> artificial

<220>

<223> Sequencing primer for TOPO-pCRII: bases 434-458

<400> 25

cgccagggtt ttcccagtca cgac

24

<210> 26
<211> 17
<212> DNA
<213> artificial

<220>

<223> M13 reverse sequencing primer for TOPO-pCRII: bases 205-222

<400> 26

caggaaacag ctatgac

17

<210> 27
<211> 20
<212> DNA
<213> artificial

<220>

<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases
1989-2008

<400> 27

cagggacgag aagaggctta

20

<210> 28
<211> 19
<212> DNA
<213> artificial

<220>

<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases
1513-1531

<400> 28

acaccagagc agctctatg

19

<210> 29
<211> 24
<212> DNA
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<220>
 <223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases
 2399-2422

 <400> 29
 tagcaccaat cagtgaagaa gagc 24

 <210> 30
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 322-343

 <400> 30
 gccagtgata tggtacacag tg 22

 <210> 31
 <211> 24
 <212> DNA
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 <220>
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 140-163

 <400> 31
 taacaggtca ctatggaaca cacg 24

 <210> 32
 <211> 24
 <212> DNA
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 <220>
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 537-560

 <400> 32
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 <210> 33
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 815-835

 <400> 33

ggagtgggtga agatgatcat g 21

<210> 34
<211> 25
<212> DNA
<213> artificial

<220>
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases
993-1017

<400> 34
ccataatgtt agtggacaat atgac 25

<210> 35
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<213> artificial

<220>
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases
1073-1093

<400> 35
atgacgctgt gatgtcattg g 21

<210> 36
<211> 22
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<220>
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1673-1694

<400> 36
gatgcactga gaagcctgag ac 22

<210> 37
<211> 823
<212> PRT
<213> Human herpesvirus 8

<400> 37
Met Thr Pro Arg Ser Arg Leu Ala Thr Leu Gly Thr Val Ile Leu Leu
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20 25 30

Thr Ser Ser Ser Pro Thr Pro Pro Gly Ser Ser Ser Lys Ala Pro Thr
35 40 45

Lys Pro Gly Glu Glu Ala Ser Gly Pro Lys Ser Val Asp Phe Tyr Gln
 50 55 60
 Phe Arg Val Cys Ser Ala Ser Ile Thr Gly Glu Leu Phe Arg Phe Asn
 65 70 75 80
 Leu Glu Gln Thr Cys Pro Asp Thr Lys Asp Lys Tyr His Gln Glu Gly
 85 90 95
 Ile Leu Leu Val Tyr Lys Lys Asn Ile Val Pro His Ile Phe Lys Val
 100 105 110
 Arg Arg Tyr Arg Lys Ile Ala Thr Ser Val Thr Val Tyr Arg Gly Leu
 115 120 125
 Thr Glu Ser Ala Ile Thr Asn Lys Tyr Glu Leu Pro Arg Pro Val Pro
 130 135 140
 Leu Tyr Glu Ile Ser His Met Asp Ser Thr Tyr Gln Cys Phe Ser Ser
 145 150 155 160
 Met Lys Val Asn Val Asn Gly Val Glu Asn Thr Phe Thr Asp Arg Asp
 165 170 175
 Asp Val Asn Thr Thr Val Phe Leu Gln Pro Val Glu Gly Leu Thr Asp
 180 185 190
 Asn Ile Gln Arg Tyr Phe Ser Gln Pro Val Ile Tyr Ala Glu Pro Gly
 195 200 205
 Trp Phe Pro Gly Ile Tyr Arg Val Arg Thr Thr Val Asn Cys Glu Ile
 210 215 220
 Val Asp Met Ile Ala Arg Ser Ala Glu Pro Tyr Asn Tyr Phe Val Thr
 225 230 235 240
 Ser Leu Gly Asp Thr Val Glu Val Ser Pro Phe Cys Tyr Asn Glu Ser
 245 250 255
 Ser Cys Ser Thr Thr Pro Ser Asn Lys Asn Gly Leu Ser Val Gln Val
 260 265 270
 Val Leu Asn His Thr Val Val Thr Tyr Ser Asp Arg Gly Thr Ser Pro
 275 280 285
 Thr Pro Gln Asn Arg Ile Phe Val Glu Thr Gly Ala Tyr Thr Leu Ser
 290 295 300
 Trp Ala Ser Glu Ser Lys Thr Thr Ala Val Cys Pro Leu Ala Leu Trp
 305 310 315 320
 Lys Thr Phe Pro Arg Ser Ile Gln Thr Thr His Glu Asp Ser Phe His
 325 330 335
 Phe Val Ala Asn Glu Ile Thr Ala Thr Phe Thr Ala Pro Leu Thr Pro
 340 345 350

Val	Ala	Asn	Phe	Thr	Asp	Thr	Tyr	Ser	Cys	Leu	Thr	Ser	Asp	Ile	Asn		
		355					360					365					
Thr	Thr	Leu	Asn	Ala	Ser	Lys	Ala	Lys	Leu	Ala	Ser	Thr	His	Val	Pro		
		370				375						380					
Asn	Gly	Thr	Val	Gln	Tyr	Phe	His	Thr	Thr	Gly	Gly	Leu	Tyr	Leu	Val		
385					390					395					400		
Trp	Gln	Pro	Met	Ser	Ala	Ile	Asn	Leu	Thr	His	Ala	Gln	Gly	Asp	Ser		
				405					410					415			
Gly	Asn	Pro	Thr	Ser	Ser	Pro	Pro	Pro	Ser	Ala	Ser	Pro	Met	Thr	Thr		
			420					425					430				
Ser	Ala	Ser	Arg	Arg	Lys	Arg	Arg	Ser	Ala	Ser	Thr	Ala	Ala	Ala	Gly		
		435					440					445					
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	450					455					460						
Tyr	Asp	Lys	Leu	Arg	Asp	Gly	Ile	Asn	Gln	Val	Leu	Glu	Glu	Leu	Ser		
465					470					475					480		
Arg	Ala	Trp	Cys	Arg	Glu	Gln	Val	Arg	Asp	Asn	Leu	Met	Trp	Tyr	Glu		
				485					490					495			
Leu	Ser	Lys	Ile	Asn	Pro	Thr	Ser	Val	Met	Thr	Ala	Ile	Tyr	Gly	Arg		
			500					505					510				
Pro	Val	Ser	Ala	Lys	Phe	Val	Gly	Asp	Ala	Ile	Ser	Val	Thr	Glu	Cys		
		515					520					525					
Ile	Asn	Val	Asp	Gln	Ser	Ser	Val	Asn	Ile	His	Lys	Ser	Leu	Arg	Thr		
	530					535					540						
Asn	Ser	Lys	Asp	Val	Cys	Tyr	Ala	Arg	Pro	Leu	Val	Thr	Phe	Lys	Phe		
545					550					555					560		
Leu	Asn	Ser	Ser	Asn	Leu	Phe	Thr	Gly	Gln	Leu	Gly	Ala	Arg	Asn	Glu		
				565					570					575			
Ile	Ile	Leu	Thr	Asn	Asn	Gln	Val	Glu	Thr	Cys	Lys	Asp	Thr	Cys	Glu		
			580					585					590				
His	Tyr	Phe	Ile	Thr	Arg	Asn	Glu	Thr	Leu	Val	Tyr	Lys	Asp	Tyr	Ala		
		595				600						605					
Tyr	Leu	Arg	Thr	Ile	Asn	Thr	Thr	Asp	Ile	Ser	Thr	Leu	Asn	Thr	Phe		
	610					615					620						
Ile	Ala	Leu	Asn	Leu	Ser	Phe	Ile	Gln	Asn	Ile	Asp	Phe	Lys	Ala	Ile		
625					630					635					640		
Glu	Leu	Tyr	Ser	Ser	Ala	Glu	Lys	Arg	Leu	Ala	Ser	Ser	Val	Phe	Asp		
				645					650					655			

Leu Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Thr His Arg Leu Ala
 660 665 670
 Gly Leu Arg Glu Asp Leu Asp Asn Thr Ile Asp Met Asn Lys Glu Arg
 675 680 685
 Phe Val Arg Asp Leu Ser Glu Ile Val Ala Asp Leu Gly Gly Ile Gly
 690 695 700
 Lys Thr Val Val Asn Val Ala Ser Ser Val Val Thr Leu Cys Gly Ser
 705 710 715 720
 Leu Val Thr Gly Phe Ile Asn Phe Ile Lys His Pro Leu Gly Gly Met
 725 730 735
 Leu Met Ile Ile Ile Val Ile Ala Ile Ile Leu Ile Ile Phe Met Leu
 740 745 750
 Ser Arg Arg Thr Asn Thr Ile Ala Gln Ala Pro Val Lys Met Ile Tyr
 755 760 765
 Pro Asp Val Asp Arg Arg Ala Pro Pro Ser Gly Gly Ala Pro Thr Arg
 770 775 780
 Glu Glu Ile Lys Asn Ile Leu Leu Gly Met His Gln Leu Gln Gln Glu
 785 790 795 800
 Arg Gln Lys Ala Asp Asp Leu Lys Lys Ser Thr Pro Ser Val Phe Gln
 805 810 815
 Arg Thr Ala Asn Gly Leu Arg
 820
 <210> 38
 <211> 808
 <212> PRT
 <213> Rhesus monkey rhadinovirus
 <400> 38
 Met Met Ile Thr Asn Arg Thr Arg Arg Leu Leu Arg Ala Trp Val Val
 1 5 10 15
 Ile Ile Ala Ile Gly Thr Ala Val Gly Glu Asn Val Thr Thr Pro Lys
 20 25 30
 Gly Ala Thr Thr Thr Ala Lys Pro Thr Pro Gly Pro Ser Thr Pro Thr
 35 40 45
 Pro Pro Glu Asn Pro Pro Arg Ala Glu Ala Phe Lys Phe Arg Val Cys
 50 55 60
 Ser Ala Ser Ala Thr Gly Glu Leu Phe Arg Phe Asn Leu Glu Lys Thr
 65 70 75 80
 Cys Pro Gly Thr Glu Asp Lys Thr His Gln Glu Gly Ile Leu Met Val
 85 90 95

Phe	Lys	Lys	Asn	Ile	Val	Pro	His	Ile	Phe	Lys	Val	Arg	Arg	Tyr	Arg		
			100					105						110			
Lys	Val	Ala	Thr	Ser	Val	Thr	Val	Tyr	Arg	Gly	Trp	Thr	Glu	Thr	Ala		
		115					120					125					
Val	Thr	Gly	Lys	Gln	Glu	Val	Ile	Arg	Pro	Val	Pro	Gln	Tyr	Glu	Ile		
	130					135					140						
Asn	His	Met	Asp	Thr	Thr	Tyr	Gln	Cys	Phe	Ser	Ser	Met	Arg	Val	Asn		
145					150					155					160		
Val	Asn	Gly	Ile	Val	Asn	Thr	Tyr	Thr	Asp	Arg	Asp	Phe	Thr	Asn	Gln		
			165						170					175			
Thr	Val	Phe	Leu	Gln	Pro	Val	Glu	Gly	Leu	Thr	Asp	Asn	Ile	Gln	Arg		
		180						185					190				
Tyr	Phe	Ser	Gln	Pro	Val	Leu	Tyr	Thr	Thr	Pro	Gly	Trp	Phe	Pro	Gly		
		195					200					205					
Ile	Tyr	Arg	Val	Arg	Thr	Thr	Val	Asn	Cys	Glu	Ile	Val	Asp	Met	Ile		
	210					215					220						
Ala	Arg	Ser	Ala	Glu	Pro	Tyr	Ser	Tyr	Phe	Val	Thr	Ala	Leu	Gly	Asp		
225					230					235					240		
Thr	Val	Glu	Val	Ser	Pro	Phe	Cys	His	Asn	Asp	Ser	Thr	Cys	Ser	Val		
			245					250						255			
Ala	Glu	Lys	Thr	Glu	Asn	Gly	Leu	Gly	Ala	Arg	Val	Leu	Thr	Asn	Tyr		
			260					265						270			
Thr	Met	Val	Asp	Phe	Ala	Thr	Arg	Ala	Pro	Thr	Thr	Glu	Thr	Arg	Val		
	275						280					285					
Phe	Ala	Asp	Ser	Gly	Glu	Tyr	Thr	Val	Ser	Trp	Lys	Ala	Glu	Asp	Pro		
	290					295					300						
Lys	Ser	Ala	Val	Cys	Ala	Leu	Thr	Leu	Trp	Lys	Thr	Phe	Pro	Arg	Ala		
305					310					315					320		
Ile	Gln	Thr	Thr	His	Glu	Ala	Ser	Tyr	His	Phe	Val	Ala	Asn	Asp	Val		
				325					330					335			
Thr	Ala	Thr	Phe	Thr	Ser	Pro	Leu	Ser	Glu	Val	Ala	Asn	Phe	Thr	Gly		
		340						345					350				
Thr	Tyr	Ser	Cys	Leu	Asp	Glu	Val	Ile	Gln	Lys	Thr	Leu	Asn	Asp	Thr		
		355					360					365					
Ile	Lys	Lys	Leu	Ser	Asp	Thr	His	Val	Thr	Asn	Gly	Ser	Ala	Gln	Tyr		
	370					375					380						
Tyr	Lys	Thr	Glu	Gly	Gly	Leu	Phe	Leu	Leu	Trp	Gln	Pro	Leu	Thr	Pro		
385					390					395					400		

Leu Ser Leu Val Asp Glu Met Arg Gly Leu Asn Gly Thr Thr Pro Ala
 405 410 415
 Pro Pro Ala Thr Thr Ser Thr Val Ser Arg Val Arg Arg Ser Val Asn
 420 425 430
 Thr Asn Glu Gln Ala Thr Asp Asn Leu Ala Ala Pro Gln Leu Gln Phe
 435 440 445
 Ala Tyr Asp Lys Leu Arg Ala Ser Ile Asn Lys Val Leu Glu Glu Leu
 450 455 460
 Ser Arg Ala Trp Cys Arg Glu Gln Val Arg Asp Thr Tyr Met Trp Tyr
 465 470 475 480
 Glu Leu Ser Lys Ile Asn Pro Thr Ser Val Met Thr Ala Ile Tyr Gly
 485 490 495
 Arg Pro Val Ser Ala Lys Phe Val Gly Asp Ala Ile Ser Val Thr Asp
 500 505 510
 Cys Val Ala Val Asp Gln Ala Ser Val Ser Ile His Lys Ser Leu Arg
 515 520 525
 Thr Ser Thr Pro Gly Met Cys Tyr Ser Arg Pro Pro Val Thr Phe Arg
 530 535 540
 Phe Leu Asn Ser Thr Thr Leu Phe Lys Gly Gln Leu Gly Pro Arg Asn
 545 550 555 560
 Glu Ile Ile Leu Thr Asp Asn Gln Val Glu Ala Cys Lys Glu Thr Cys
 565 570 575
 Glu His Tyr Phe Ile Ala Ser Asn Val Thr Tyr Tyr Tyr Lys Asp Tyr
 580 585 590
 Val Phe Val Lys Lys Ile Asn Thr Ser Glu Ile Ser Thr Leu Gly Thr
 595 600 605
 Phe Ile Ala Leu Asn Leu Ser Phe Ile Glu Asn Ile Asp Phe Arg Val
 610 615 620
 Ile Glu Leu Tyr Ser Arg Ala Glu Lys Lys Leu Ser Gly Ser Val Phe
 625 630 635 640
 Asp Ile Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Thr Gln Arg Leu
 645 650 655
 Ala Gly Leu Arg Glu Asp Leu Asp Asn Thr Ile Asp Leu Asn Arg Asp
 660 665 670
 Arg Leu Ala Arg Asp Leu Ser Glu Ile Val Ala Asp Leu Gly Asp Val
 675 680 685
 Gly Arg Thr Val Val Asn Val Ala Ser Ser Val Ile Thr Leu Phe Gly
 690 695 700

Ser Ile Val Ser Gly Phe Ile Asn Phe Ile Lys Ser Pro Phe Gly Gly
 705 710 715 720
 Met Leu Met Ile Leu Val Ile Val Ala Val Val Leu Ile Val Phe Ala
 725 730 735
 Leu Asn Arg Arg Thr Asn Ala Ile Ala Gln Ala Pro Ile Arg Met Ile
 740 745 750
 Tyr Pro Asp Ile Asp Lys Met Gln Pro Ser Gly Gly Lys Val Asp Gln
 755 760 765
 Glu Gln Ile Lys Asn Ile Leu Ala Gly Met His Gln Leu Gln Gln Glu
 770 775 780
 Glu Arg Arg Arg Leu Asp Glu Gln Gln Arg Ser Ala Pro Ser Leu Phe
 785 790 795 800
 Arg Arg Ala Ser Asp Gly Leu Lys
 805

<210> 39
 <211> 831
 <212> PRT
 <213> Murine herpesvirus 68

<400> 39
 Met Tyr Pro Thr Val Lys Ser Met Arg Val Ala His Leu Thr Asn Leu
 1 5 10 15
 Leu Thr Leu Leu Cys Leu Leu Cys His Thr His Leu Tyr Val Cys Gln
 20 25 30
 Pro Thr Thr Leu Arg Gln Pro Ser Asp Met Thr Pro Ala Gln Asp Ala
 35 40 45
 Pro Thr Glu Thr Pro Pro Pro Leu Ser Thr Asn Thr Asn Arg Gly Phe
 50 55 60
 Glu Tyr Phe Arg Val Cys Gly Val Ala Ala Thr Gly Glu Thr Phe Arg
 65 70 75 80
 Phe Asp Leu Asp Lys Thr Cys Pro Ser Thr Gln Asp Lys Lys His Val
 85 90 95
 Glu Gly Ile Leu Leu Val Tyr Lys Ile Asn Ile Val Pro Tyr Ile Phe
 100 105 110
 Lys Ile Arg Arg Tyr Arg Lys Ile Ile Thr Gln Leu Thr Ile Trp Arg
 115 120 125
 Gly Leu Thr Thr Ser Ser Val Thr Gly Lys Phe Glu Met Ala Thr Gln
 130 135 140
 Ala His Glu Trp Glu Val Gly Asp Phe Asp Ser Ile Tyr Gln Cys Tyr
 145 150 155 160

Asn Ser Ala Thr Met Val Val Asn Asn Val Arg Gln Val Tyr Val Asp
 165 170 175
 Arg Asp Gly Val Asn Lys Thr Val Asn Ile Arg Pro Val Asp Gly Leu
 180 185 190
 Thr Gly Asn Ile Gln Arg Tyr Phe Ser Gln Pro Thr Leu Tyr Ser Glu
 195 200 205
 Pro Gly Trp Met Pro Gly Phe Tyr Arg Val Arg Thr Thr Val Asn Cys
 210 215 220
 Glu Ile Val Asp Met Val Ala Arg Ser Met Asp Pro Tyr Asn Tyr Ile
 225 230 235 240
 Ala Thr Ala Leu Gly Asp Ser Leu Glu Leu Ser Pro Phe Gln Thr Phe
 245 250 255
 Asp Asn Thr Ser Gln Ser Thr Ala Pro Lys Arg Ala Asp Met Arg Val
 260 265 270
 Arg Glu Val Lys Asn Tyr Lys Phe Val Asp Tyr Asn Asn Arg Gly Thr
 275 280 285
 Ala Pro Ala Gly Gln Ser Arg Thr Phe Leu Glu Thr Pro Ser Ala Thr
 290 295 300
 Tyr Ser Trp Lys Thr Ala Thr Arg Gln Thr Ala Thr Cys Asp Leu Val
 305 310 315 320
 His Trp Lys Thr Phe Pro Arg Ala Ile Gln Thr Ala His Glu His Ser
 325 330 335
 Tyr His Phe Val Ala Asn Glu Val Thr Ala Thr Phe Asn Thr Pro Leu
 340 345 350
 Thr Glu Val Glu Asn Phe Thr Ser Thr Tyr Ser Cys Val Ser Asp Gln
 355 360 365
 Ile Asn Lys Thr Ile Ser Glu Tyr Ile Gln Lys Leu Asn Asn Ser Tyr
 370 375 380
 Val Ala Ser Gly Lys Thr Gln Tyr Phe Lys Thr Asp Gly Asn Leu Tyr
 385 390 395 400
 Leu Ile Trp Gln Pro Leu Glu His Pro Glu Ile Glu Asp Ile Asp Glu
 405 410 415
 Asp Ser Asp Pro Glu Pro Thr Pro Ala Pro Pro Lys Ser Thr Arg Arg
 420 425 430
 Lys Arg Glu Ala Ala Asp Asn Gly Asn Ser Thr Ser Glu Val Ser Lys
 435 440 445
 Gly Ser Glu Asn Pro Leu Ile Thr Ala Gln Ile Gln Phe Ala Tyr Asp
 450 455 460

Lys	Leu	Thr	Thr	Ser	Val	Asn	Asn	Val	Leu	Glu	Glu	Leu	Ser	Arg	Ala	
465					470					475					480	
Trp	Cys	Arg	Glu	Gln	Val	Arg	Asp	Thr	Leu	Met	Trp	Tyr	Glu	Leu	Ser	
			485						490					495		
Lys	Val	Asn	Pro	Thr	Ser	Val	Met	Ser	Ala	Ile	Tyr	Gly	Lys	Pro	Val	
			500					505					510			
Ala	Ala	Arg	Tyr	Val	Gly	Asp	Ala	Ile	Ser	Val	Thr	Asp	Cys	Ile	Tyr	
		515					520					525				
Val	Asp	Gln	Ser	Ser	Val	Asn	Ile	His	Gln	Ser	Leu	Arg	Leu	Gln	His	
	530					535					540					
Asp	Lys	Thr	Thr	Cys	Tyr	Ser	Arg	Pro	Arg	Val	Thr	Phe	Lys	Phe	Ile	
545				550						555					560	
Asn	Ser	Thr	Asp	Pro	Leu	Thr	Gly	Gln	Leu	Gly	Pro	Arg	Lys	Glu	Ile	
			565						570					575		
Ile	Leu	Ser	Asn	Thr	Asn	Ile	Glu	Thr	Cys	Lys	Asp	Glu	Ser	Glu	His	
			580					585						590		
Tyr	Phe	Ile	Val	Gly	Glu	Tyr	Ile	Tyr	Tyr	Tyr	Lys	Asn	Tyr	Ile	Phe	
		595					600					605				
Glu	Glu	Lys	Leu	Asn	Leu	Ser	Ser	Ile	Ala	Thr	Leu	Asp	Thr	Phe	Ile	
	610					615					620					
Ala	Leu	Asn	Ile	Ser	Phe	Ile	Glu	Asn	Ile	Asp	Phe	Lys	Thr	Val	Glu	
625					630					635					640	
Leu	Tyr	Ser	Ser	Thr	Glu	Arg	Lys	Leu	Ala	Ser	Ser	Val	Phe	Asp	Ile	
				645					650					655		
Glu	Ser	Met	Phe	Arg	Glu	Tyr	Asn	Tyr	Tyr	Thr	Tyr	Ser	Leu	Ala	Gly	
			660					665					670			
Ile	Lys	Lys	Asp	Leu	Asp	Asn	Thr	Ile	Asp	Tyr	Asn	Arg	Asp	Arg	Leu	
		675					680					685				
Val	Gln	Asp	Leu	Ser	Asp	Met	Met	Ala	Asp	Leu	Gly	Asp	Ile	Gly	Arg	
	690					695					700					
Ser	Val	Val	Asn	Val	Val	Ser	Ser	Val	Val	Thr	Phe	Phe	Ser	Ser	Ile	
705					710					715					720	
Val	Thr	Gly	Phe	Ile	Lys	Phe	Phe	Thr	Asn	Pro	Leu	Gly	Gly	Ile	Phe	
			725						730					735		
Ile	Leu	Leu	Ile	Ile	Gly	Gly	Ile	Ile	Phe	Leu	Val	Val	Val	Leu	Asn	
			740					745						750		
Arg	Arg	Asn	Ser	Gln	Phe	His	Asp	Ala	Pro	Ile	Lys	Met	Leu	Tyr	Pro	
		755					760					765				

Ser Val Glu Asn Tyr Ala Ala Arg Gln Ala Pro Pro Pro Tyr Ser Ala
 770 775 780

Ser Pro Pro Ala Ile Asp Lys Glu Glu Ile Lys Arg Ile Leu Leu Gly
 785 790 795 800

Met His Gln Val His Gln Glu Glu Lys Glu Ala Gln Lys Gln Leu Thr
 805 810 815

Asn Ser Gly Pro Thr Leu Trp Gln Lys Ala Thr Gly Phe Leu Arg
 820 825 830

<210> 40
 <211> 844
 <212> PRT
 <213> Bovine herpesvirus 4

<400> 40
 Tyr Tyr Lys Thr Ile Leu Phe Phe Ala Leu Ile Lys Val Cys Ser Phe
 1 5 10 15

Asn Gln Thr Thr Thr His Ser Thr Thr Thr Ser Pro Ser Ile Ser Ser
 20 25 30

Thr Thr Ser Ser Thr Thr Thr Ser Thr Ser Lys Pro Ser Asn Thr Thr
 35 40 45

Ser Thr Asn Ser Ser Leu Ala Ala Ser Pro Gln Asn Thr Ser Thr Ser
 50 55 60

Lys Pro Ser Thr Asp Asn Gln Gly Thr Ser Thr Pro Thr Ile Pro Thr
 65 70 75 80

Val Thr Asp Asp Thr Ala Ser Lys Asn Phe Tyr Lys Tyr Arg Val Cys
 85 90 95

Ser Ala Ser Ser Ser Ser Gly Glu Leu Phe Arg Phe Asp Leu Asp Gln
 100 105 110

Thr Cys Pro Asp Thr Lys Asp Lys Lys His Val Glu Gly Ile Leu Leu
 115 120 125

Val Leu Lys Lys Asn Ile Val Pro Tyr Ile Phe Lys Val Arg Lys Tyr
 130 135 140

Arg Lys Ile Ala Thr Ser Val Thr Val Tyr Arg Gly Trp Ser Gln Ala
 145 150 155 160

Ala Val Thr Asn Arg Asp Asp Ile Ser Arg Ala Ile Pro Tyr Asn Glu
 165 170 175

Ile Ser Met Ile Asp Arg Thr Tyr His Cys Phe Ser Ala Met Ala Thr
 180 185 190

Val Ile Asn Gly Ile Leu Asn Thr Tyr Ile Asp Arg Asp Ser Glu Asn
 195 200 205

Lys Ser Val Pro Leu Gln Pro Val Ala Gly Leu Thr Glu Asn Ile Asn
 210 215 220
 Arg Tyr Phe Ser Gln Pro Leu Ile Tyr Ala Glu Pro Gly Trp Phe Pro
 225 230 235 240
 Gly Ile Tyr Arg Val Arg Thr Thr Val Asn Cys Glu Val Val Asp Met
 245 250 255
 Tyr Ala Arg Ser Val Glu Pro Tyr Thr His Phe Ile Thr Ala Leu Gly
 260 265 270
 Asp Thr Ile Glu Ile Ser Pro Phe Cys His Asn Asn Ser Gln Cys Thr
 275 280 285
 Thr Gly Asn Ser Thr Ser Arg Asp Ala Thr Lys Val Trp Ile Glu Glu
 290 295 300
 Asn His Gln Thr Val Asp Tyr Glu Arg Arg Gly His Pro Thr Lys Asp
 305 310 315 320
 Lys Arg Ile Phe Leu Lys Asp Glu Glu Tyr Thr Ile Ser Trp Lys Ala
 325 330 335
 Glu Asp Arg Glu Arg Ala Ile Cys Asp Phe Val Ile Trp Lys Thr Phe
 340 345 350
 Pro Arg Ala Ile Gln Thr Ile His Asn Glu Ser Phe His Phe Val Ala
 355 360 365
 Asn Glu Val Thr Ala Ser Phe Leu Thr Ser Asn Gln Glu Glu Thr Glu
 370 375 380
 Leu Arg Gly Asn Thr Glu Ile Leu Asn Cys Met Asn Ser Thr Ile Asn
 385 390 395 400
 Glu Thr Leu Glu Glu Thr Val Lys Lys Phe Asn Lys Ser His Ile Arg
 405 410 415
 Asp Gly Glu Val Lys Tyr Tyr Lys Thr Asn Gly Gly Leu Phe Leu Ile
 420 425 430
 Trp Gln Ala Met Lys Pro Leu Asn Leu Ser Glu His Thr Asn Tyr Thr
 435 440 445
 Ile Glu Arg Asn Asn Lys Thr Gly Asn Lys Ser Arg Gln Lys Arg Ser
 450 455 460
 Val Asp Thr Lys Thr Phe Gln Gly Ala Lys Gly Leu Ser Thr Ala Gln
 465 470 475 480
 Val Gln Tyr Ala Tyr Asp His Leu Arg Thr Ser Met Asn His Ile Leu
 485 490 495
 Glu Glu Leu Thr Lys Thr Trp Cys Arg Glu Gln Lys Lys Asp Asn Leu
 500 505 510

Met	Trp	Tyr	Glu	Leu	Ser	Lys	Ile	Asn	Pro	Val	Ser	Val	Met	Ala	Ala		
			515					520				525					
Ile	Tyr	Gly	Lys	Pro	Val	Ala	Val	Lys	Ala	Met	Gly	Asp	Ala	Phe	Met		
		530				535					540						
Val	Ser	Glu	Cys	Ile	Asn	Val	Asp	Gln	Ala	Ser	Val	Asn	Ile	His	Lys		
545					550					555					560		
Ser	Met	Arg	Thr	Asp	Asp	Pro	Lys	Val	Cys	Tyr	Ser	Arg	Pro	Leu	Val		
				565					570					575			
Thr	Phe	Lys	Phe	Val	Asn	Ser	Thr	Ala	Thr	Phe	Arg	Gly	Gln	Leu	Gly		
			580					585					590				
Thr	Arg	Asn	Glu	Ile	Leu	Leu	Thr	Asn	Thr	His	Val	Glu	Thr	Cys	Arg		
		595					600					605					
Pro	Thr	Ala	Asp	His	Tyr	Phe	Phe	Val	Lys	Asn	Met	Thr	His	Tyr	Phe		
		610				615					620						
Lys	Asp	Tyr	Lys	Phe	Val	Lys	Thr	Met	Asp	Thr	Asn	Asn	Ile	Ser	Thr		
625					630					635					640		
Leu	Asp	Thr	Phe	Leu	Thr	Leu	Asn	Leu	Thr	Phe	Ile	Asp	Asn	Ile	Asp		
				645					650					655			
Phe	Lys	Thr	Val	Glu	Leu	Tyr	Ser	Glu	Thr	Glu	Arg	Lys	Met	Ala	Ser		
			660					665					670				
Ala	Leu	Asp	Leu	Glu	Thr	Met	Phe	Arg	Glu	Tyr	Asn	Tyr	Tyr	Thr	Gln		
		675					680					685					
Lys	Leu	Ala	Ser	Leu	Arg	Glu	Asp	Leu	Asp	Asn	Thr	Ile	Asp	Leu	Asn		
		690				695					700						
Arg	Asp	Arg	Leu	Val	Lys	Asp	Leu	Ser	Glu	Met	Met	Ala	Asp	Leu	Gly		
705					710					715					720		
Asp	Ile	Gly	Lys	Val	Val	Val	Asn	Thr	Phe	Ser	Gly	Ile	Val	Thr	Val		
				725					730					735			
Phe	Gly	Ser	Ile	Val	Gly	Gly	Phe	Val	Ser	Phe	Phe	Thr	Asn	Pro	Ile		
			740					745					750				
Gly	Gly	Val	Thr	Ile	Ile	Leu	Leu	Leu	Ile	Val	Val	Val	Phe	Val	Val		
		755					760					765					
Phe	Ile	Val	Ser	Arg	Arg	Thr	Asn	Asn	Met	Asn	Glu	Ala	Pro	Ile	Lys		
		770				775					780						
Met	Ile	Tyr	Pro	Asn	Ile	Asp	Lys	Ala	Ser	Glu	Gln	Glu	Asn	Ile	Gln		
785					790					795					800		
Pro	Leu	Pro	Gly	Glu	Glu	Ile	Lys	Arg	Ile	Leu	Leu	Gly	Met	His	Gln		
				805					810					815			

Leu Gln Gln Ser Glu His Gly Lys Ser Glu Glu Glu Ala Ser His Lys
820 825 830

Pro Gly Leu Phe Gln Leu Leu Gly Asp Gly Leu Gln
835 840

<210> 41

<211> 791

<212> PRT

<213> Ateline herpesvirus 3

<400> 41

Met Thr Leu Asn Arg Cys Val Leu Leu Ile Val Leu Thr Phe Ser Thr
1 5 10 15

Ala Cys Ser Gln Thr Thr Pro Ala Ser Ser Asp Glu Asn Gly Lys Thr
20 25 30

Pro Ala Ile Glu Lys Glu Tyr Phe Lys Tyr Arg Val Cys Ser Ala Ser
35 40 45

Thr Thr Gly Glu Leu Phe Arg Phe Asn Leu Asp Arg Ala Cys Pro Ser
50 55 60

Thr Glu Asp Lys Val His Arg Glu Gly Ile Leu Leu Val Tyr Lys Lys
65 70 75 80

Asn Ile Val Pro His Ile Phe Lys Val Arg Arg Tyr Lys Lys Ile Ala
85 90 95

Thr Ser Val Arg Ile Phe Asn Gly Trp Ser Arg Glu Gly Val Ala Ile
100 105 110

Thr Asn Lys Trp Glu Leu Ser Arg Ala Val Pro Lys Tyr Glu Ile Asn
115 120 125

Leu Met Asp Lys Asn Tyr Gln Cys His Asn Cys Met Gln Ile Glu Val
130 135 140

Asn Gly Leu Leu Asn Ser Tyr Cys Asp Arg Asp Gly Asn Asn Lys Thr
145 150 155 160

Val Asp Leu Lys Pro Val Asp Gly Leu Thr Gly Ala Ile Thr Arg Tyr
165 170 175

Val Ser Gln Pro Lys Ile Phe Ala Asp Ala Gly Trp Leu Trp Gly Thr
180 185 190

Tyr Lys Thr Arg Thr Thr Val Asn Cys Glu Ile Val Glu Met Phe Ala
195 200 205

Arg Ser Ala Asp Pro Tyr Thr Tyr Phe Val Thr Ala Leu Gly Asp Thr
210 215 220

Val Glu Val Ser Pro Phe Cys Asp Ala Glu Asn Ser Cys Pro Asn Ala
225 230 235 240

Ser Asp Val Leu Ser Ser Gln Val Asp Phe Asn His Thr Val Val Asp
 245 250 255
 Tyr Gly Asn Arg Ala Thr Ser Gln Gln His Gly Lys Arg Ile Phe Ala
 260 265 270
 His Thr Leu Asp Tyr Ser Val Ser Trp Glu Ala Ile Asn Lys Thr Thr
 275 280 285
 Ser Val Cys Ser Met Val Phe Trp Lys Gly Phe Gln Arg Ala Ile Gln
 290 295 300
 Thr Glu His Asp Ser Thr Tyr His Phe Ile Ala Asn Glu Ile Thr Ala
 305 310 315 320
 Gly Phe Ser Thr Ser Lys Glu Thr Leu Ala Ser Phe Ser Ser Glu Tyr
 325 330 335
 Ser Cys Leu Met Ser Asp Ile Asn Ser Thr Leu Thr Asp Lys Ile Gly
 340 345 350
 Arg Val Asn Asn Thr His Val Pro Asn Gly Thr Ala Gln Tyr Phe Lys
 355 360 365
 Thr Glu Gly Gly Met Ile Leu Val Trp Gln Pro Leu Thr Ala Ile Glu
 370 375 380
 Leu Glu Glu Ala Met Ile Glu Ala Thr Thr Val Ser Pro Thr Pro Leu
 385 390 395 400
 Ser Thr Ala His Leu Thr Ser Arg Arg Thr Gly Arg Arg Lys Arg Asp
 405 410 415
 Val Ser Ala Gly Ser Glu Asn Ser Val Leu Leu Ala Gln Ile Gln Tyr
 420 425 430
 Ala Tyr Asp Lys Leu Arg Gln Ser Ile Asn Asn Val Leu Glu Glu Leu
 435 440 445
 Ala Ile Thr Trp Cys Arg Glu Gln Val Arg Gln Thr Met Ile Trp Tyr
 450 455 460
 Glu Ile Ala Lys Ile Asn Pro Thr Ser Val Met Thr Ala Ile Tyr Gly
 465 470 475 480
 Lys Pro Val Ser Ala Lys Ala Leu Gly Asp Val Ile Ser Val Thr Glu
 485 490 495
 Cys Ile Asn Val Asp Gln Thr Ser Val Ser Ile His Lys Ser Leu Lys
 500 505 510
 Thr Thr Asn Asn Asp Val Cys Tyr Ser Arg Pro Pro Val Thr Phe Lys
 515 520 525
 Phe Val Asn Ser Ser Gln Leu Phe Lys Gly Gln Leu Gly Ala Arg Asn
 530 535 540

Glu Ile Leu Leu Ser Glu Ser Leu Val Glu Asn Cys His Gln Asn Ala
 545 550 555 560
 Glu His Phe Phe Thr Ala Lys Asn Glu Thr Tyr His Phe Lys Asn Tyr
 565 570 575
 Leu His Val Glu Thr Leu Pro Leu Thr Asn Ile Ser Thr Leu Asp Thr
 580 585 590
 Phe Leu Ala Leu Asn Leu Thr Phe Ile Glu Asn Ile Asp Phe Lys Ala
 595 600 605
 Val Glu Leu Tyr Ser Ser Gly Glu Arg Lys Leu Ala Asn Val Phe Asp
 610 615 620
 Leu Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Ala Gln Ser Ile Ser
 625 630 635 640
 Gly Leu Arg Lys Asp Phe Asp Asn Ser Gln Arg Asn Asn Arg Asp Arg
 645 650 655
 Ile Ile Gln Asp Phe Ser Glu Ile Leu Ala Asp Leu Gly Ser Ile Gly
 660 665 670
 Lys Val Ile Val Asn Ile Ala Ser Ser Ala Phe Ser Leu Phe Gly Gly
 675 680 685
 Ile Val Thr Gly Ile Leu Asn Phe Ile Lys Asn Pro Leu Gly Gly Met
 690 695 700
 Leu Thr Phe Leu Leu Val Gly Ala Ile Ile Ile Leu Val Ile Leu Leu
 705 710 715 720
 Val Arg Arg Thr Asn Asn Met Ser Gln Ala Pro Ile Arg Met Ile Tyr
 725 730 735
 Pro Asp Ile Glu Lys Ser Arg Ser Ser Val Thr Pro Thr Glu Pro Glu
 740 745 750
 Val Ile Lys Gln Ile Leu Leu Gly Met His Asn Met Gln Gln Glu Glu
 755 760 765
 Tyr Lys Lys Arg Glu Glu His Lys Ala Ser Gln Pro Ser Phe Leu Lys
 770 775 780
 Arg Ala Thr Asp Ala Phe Leu
 785 790
 <210> 42
 <211> 792
 <212> PRT
 <213> Herpesvirus saimiri
 <400> 42
 Met Val Pro Asn Lys His Leu Leu Leu Ile Ile Leu Ser Phe Ser Thr
 1 5 10 15

Ala	Cys	Gly	Gln	Thr	Thr	Pro	Thr	Thr	Ala	Val	Glu	Lys	Asn	Lys	Thr	20	25	30	
Gln	Ala	Ile	Tyr	Gln	Glu	Tyr	Phe	Lys	Tyr	Arg	Val	Cys	Ser	Ala	Ser	35	40	45	
Thr	Thr	Gly	Glu	Leu	Phe	Arg	Phe	Asp	Leu	Asp	Arg	Thr	Cys	Pro	Ser	50	55	60	
Thr	Glu	Asp	Lys	Val	His	Lys	Glu	Gly	Ile	Leu	Leu	Val	Tyr	Lys	Lys	65	70	75	80
Asn	Ile	Val	Pro	Tyr	Ile	Phe	Lys	Val	Arg	Arg	Tyr	Lys	Lys	Ile	Thr	85	90	95	
Thr	Ser	Val	Arg	Ile	Phe	Asn	Gly	Trp	Thr	Arg	Glu	Gly	Val	Ala	Ile	100	105	110	
Thr	Asn	Lys	Trp	Glu	Leu	Ser	Arg	Ala	Val	Pro	Lys	Tyr	Glu	Ile	Asp	115	120	125	
Ile	Met	Asp	Lys	Thr	Tyr	Gln	Cys	His	Asn	Cys	Met	Gln	Ile	Glu	Val	130	135	140	
Asn	Gly	Met	Leu	Asn	Ser	Tyr	Tyr	Asp	Arg	Asp	Gly	Asn	Asn	Lys	Thr	145	150	155	160
Val	Asp	Leu	Lys	Pro	Val	Asp	Gly	Leu	Thr	Gly	Ala	Ile	Thr	Arg	Tyr	165	170	175	
Ile	Ser	Gln	Pro	Lys	Val	Phe	Ala	Asp	Pro	Gly	Trp	Leu	Trp	Gly	Thr	180	185	190	
Tyr	Arg	Thr	Arg	Thr	Thr	Val	Asn	Cys	Glu	Ile	Val	Asp	Met	Phe	Ala	195	200	205	
Arg	Ser	Ala	Asp	Pro	Tyr	Thr	Tyr	Phe	Val	Thr	Ala	Leu	Gly	Asp	Thr	210	215	220	
Val	Glu	Val	Ser	Pro	Phe	Cys	Asp	Val	Asp	Asn	Ser	Cys	Pro	Asn	Ala	225	230	235	240
Thr	Asp	Val	Leu	Ser	Val	Gln	Ile	Asp	Leu	Asn	His	Thr	Val	Val	Asp	245	250	255	
Tyr	Gly	Asn	Arg	Ala	Thr	Ser	Gln	Gln	His	Lys	Lys	Arg	Ile	Phe	Ala	260	265	270	
His	Thr	Leu	Asp	Tyr	Ser	Val	Ser	Trp	Glu	Ala	Val	Asn	Lys	Ser	Ala	275	280	285	
Ser	Val	Cys	Ser	Met	Val	Phe	Trp	Lys	Ser	Phe	Gln	Arg	Ala	Ile	Gln	290	295	300	
Thr	Glu	His	Asp	Leu	Thr	Tyr	His	Phe	Ile	Ala	Asn	Glu	Ile	Thr	Ala	305	310	315	320

Gly Phe Ser Thr Val Lys Glu Pro Leu Ala Asn Phe Thr Ser Asp Tyr
 325 330 335
 Asn Cys Leu Met Thr His Ile Asn Thr Thr Leu Glu Asp Lys Ile Ala
 340 345 350
 Arg Val Asn Asn Thr His Thr Pro Asn Gly Thr Ala Glu Tyr Tyr Gln
 355 360 365
 Thr Glu Gly Gly Met Ile Leu Val Trp Gln Pro Leu Ile Ala Ile Glu
 370 375 380
 Leu Glu Glu Ala Met Leu Glu Ala Thr Thr Ser Pro Val Thr Pro Ser
 385 390 395 400
 Ala Pro Thr Ser Ser Ser Arg Ser Lys Arg Ala Ile Arg Ser Ile Arg
 405 410 415
 Asp Val Ser Ala Gly Ser Glu Asn Asn Val Phe Leu Ser Gln Ile Gln
 420 425 430
 Tyr Ala Tyr Asp Lys Leu Arg Gln Ser Ile Asn Asn Val Leu Glu Glu
 435 440 445
 Leu Ala Ile Thr Trp Cys Arg Glu Gln Val Arg Gln Thr Met Val Trp
 450 455 460
 Tyr Glu Ile Ala Lys Ile Asn Pro Thr Ser Val Met Thr Ala Ile Tyr
 465 470 475 480
 Gly Lys Pro Val Ser Arg Lys Ala Leu Gly Asp Val Ile Ser Val Thr
 485 490 495
 Glu Cys Ile Asn Val Asp Gln Ser Ser Val Ser Ile His Lys Ser Leu
 500 505 510
 Lys Thr Glu Asn Asn Asp Ile Cys Tyr Ser Arg Pro Pro Val Thr Phe
 515 520 525
 Lys Phe Val Asn Ser Ser Gln Leu Phe Lys Gly Gln Leu Gly Ala Arg
 530 535 540
 Asn Glu Ile Leu Leu Ser Glu Ser Leu Val Glu Asn Cys His Gln Asn
 545 550 555 560
 Ala Glu Thr Phe Phe Thr Ala Lys Asn Glu Thr Tyr His Phe Lys Asn
 565 570 575
 Tyr Val His Val Glu Thr Leu Pro Val Asn Asn Ile Ser Thr Leu Asp
 580 585 590
 Thr Phe Leu Ala Leu Asn Leu Thr Phe Ile Glu Asn Ile Asp Phe Lys
 595 600 605
 Ala Val Glu Leu Tyr Ser Ser Gly Glu Arg Lys Leu Ala Asn Val Phe
 610 615 620

Asp Leu Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Ala Gln Ser Ile
 625 630 635 640
 Ser Gly Leu Arg Lys Asp Phe Asp Asn Ser Gln Arg Asn Asn Arg Asp
 645 650 655
 Arg Ile Ile Gln Asp Phe Ser Glu Ile Leu Ala Asp Leu Gly Ser Ile
 660 665 670
 Gly Lys Val Ile Val Asn Val Ala Ser Gly Ala Phe Ser Leu Phe Gly
 675 680 685
 Gly Ile Val Thr Gly Ile Leu Asn Phe Ile Lys Asn Pro Leu Gly Gly
 690 695 700
 Met Phe Thr Phe Leu Leu Ile Gly Ala Val Ile Ile Leu Val Ile Leu
 705 710 715 720
 Leu Val Arg Arg Thr Asn Asn Met Ser Gln Ala Pro Ile Arg Met Ile
 725 730 735
 Tyr Pro Asp Val Glu Lys Ser Lys Ser Thr Val Thr Pro Met Glu Pro
 740 745 750
 Glu Thr Ile Lys Gln Ile Leu Leu Gly Met His Asn Met Gln Gln Glu
 755 760 765
 Ala Tyr Lys Lys Lys Glu Glu Gln Arg Ala Ala Arg Pro Ser Ile Phe
 770 775 780
 Arg Gln Ala Ala Glu Thr Phe Leu
 785 790
 <210> 43
 <211> 824
 <212> PRT
 <213> Equine herpesvirus 2
 <400> 43
 Met Gly Val Gly Gly Gly Pro Arg Val Val Leu Cys Leu Trp Cys Val
 1 5 10 15
 Ala Ala Leu Leu Cys Gln Gly Val Ala Gln Glu Val Val Ala Glu Thr
 20 25 30
 Thr Thr Pro Phe Ala Thr His Arg Pro Glu Val Val Ala Glu Glu Asn
 35 40 45
 Pro Ala Asn Pro Phe Leu Pro Phe Arg Val Cys Gly Ala Ser Pro Thr
 50 55 60
 Gly Gly Glu Ile Phe Arg Phe Pro Leu Glu Glu Ser Cys Pro Asn Thr
 65 70 75 80
 Glu Asp Lys Asp His Ile Glu Gly Ile Ala Leu Ile Tyr Lys Thr Asn
 85 90 95

Ile	Val	Pro	Tyr	Val	Phe	Asn	Val	Arg	Lys	Tyr	Arg	Lys	Ile	Met	Thr	100	105	110
Ser	Thr	Thr	Ile	Tyr	Lys	Gly	Trp	Ser	Glu	Asp	Ala	Ile	Thr	Asn	Gln	115	120	125
His	Thr	Arg	Ser	Tyr	Ala	Val	Pro	Leu	Tyr	Glu	Val	Gln	Met	Met	Asp	130	135	140
His	Tyr	Tyr	Gln	Cys	Phe	Ser	Ala	Val	Gln	Val	Asn	Glu	Gly	Gly	His	145	150	155
Val	Asn	Thr	Tyr	Tyr	Asp	Arg	Asp	Gly	Trp	Asn	Glu	Thr	Ala	Phe	Leu	165	170	175
Lys	Pro	Ala	Asp	Gly	Leu	Thr	Ser	Ser	Ile	Thr	Arg	Tyr	Gln	Ser	Gln	180	185	190
Pro	Glu	Val	Tyr	Ala	Thr	Pro	Arg	Asn	Leu	Leu	Trp	Ser	Tyr	Thr	Thr	195	200	205
Arg	Thr	Thr	Val	Asn	Cys	Glu	Val	Thr	Glu	Met	Ser	Ala	Arg	Ser	Met	210	215	220
Lys	Pro	Phe	Glu	Phe	Phe	Val	Thr	Ser	Val	Gly	Asp	Thr	Ile	Glu	Met	225	230	235
Ser	Pro	Phe	Leu	Lys	Glu	Asn	Gly	Thr	Glu	Pro	Glu	Lys	Ile	Leu	Lys	245	250	255
Arg	Pro	His	Ser	Ile	Gln	Leu	Leu	Lys	Asn	Tyr	Ala	Val	Thr	Lys	Tyr	260	265	270
Gly	Val	Gly	Leu	Gly	Gln	Ala	Asp	Asn	Ala	Thr	Arg	Phe	Phe	Ala	Ile	275	280	285
Phe	Gly	Asp	Tyr	Ser	Leu	Ser	Trp	Lys	Ala	Thr	Thr	Glu	Asn	Ser	Ser	290	295	300
Tyr	Cys	Asp	Leu	Ile	Leu	Trp	Lys	Gly	Phe	Ser	Asn	Ala	Ile	Gln	Thr	305	310	315
Gln	His	Asn	Ser	Ser	Leu	His	Phe	Ile	Ala	Asn	Asp	Ile	Thr	Ala	Ser	325	330	335
Phe	Ser	Thr	Pro	Leu	Glu	Glu	Glu	Ala	Asn	Phe	Asn	Glu	Thr	Phe	Lys	340	345	350
Cys	Ile	Trp	Asn	Asn	Thr	Gln	Glu	Glu	Ile	Gln	Lys	Lys	Leu	Lys	Glu	355	360	365
Val	Glu	Lys	Thr	His	Arg	Pro	Asn	Gly	Thr	Ala	Lys	Val	Tyr	Lys	Thr	370	375	380
Thr	Gly	Asn	Leu	Tyr	Ile	Val	Trp	Gln	Pro	Leu	Ile	Gln	Ile	Asp	Leu	385	390	395

Leu Asp Thr His Ala Lys Leu Tyr Asn Leu Thr Asn Ala Thr Ala Ser
 405 410 415
 Pro Thr Ser Thr Pro Thr Thr Ser Pro Arg Arg Arg Arg Arg Asp Thr
 420 425 430
 Ser Ser Val Ser Gly Gly Gly Asn Asn Gly Asp Asn Ser Thr Lys Glu
 435 440 445
 Glu Ser Val Ala Ala Ser Gln Val Gln Phe Ala Tyr Asp Asn Leu Arg
 450 455 460
 Lys Ser Ile Asn Arg Val Leu Gly Glu Leu Ser Arg Ala Trp Cys Arg
 465 470 475 480
 Glu Gln Tyr Arg Ala Ser Leu Met Trp Tyr Glu Leu Ser Lys Ile Asn
 485 490 495
 Pro Thr Ser Val Met Ser Ala Ile Tyr Gly Arg Pro Val Ser Ala Lys
 500 505 510
 Leu Ile Gly Asp Val Val Ser Val Ser Asp Cys Ile Ser Val Asp Gln
 515 520 525
 Lys Ser Val Phe Val His Lys Asn Met Lys Val Pro Gly Lys Glu Asp
 530 535 540
 Leu Cys Tyr Thr Arg Pro Val Val Gly Phe Lys Phe Ile Asn Gly Ser
 545 550 555 560
 Glu Leu Phe Ala Gly Gln Leu Gly Pro Arg Asn Glu Ile Val Leu Ser
 565 570 575
 Thr Ser Gln Val Glu Val Cys Gln His Ser Cys Glu His Tyr Phe Gln
 580 585 590
 Ala Gly Asn Gln Met Tyr Lys Tyr Lys Asp Tyr Tyr Tyr Val Ser Thr
 595 600 605
 Leu Asn Leu Thr Asp Ile Pro Thr Leu His Thr Met Ile Thr Leu Asn
 610 615 620
 Leu Ser Leu Val Glu Asn Ile Asp Phe Lys Val Ile Glu Leu Tyr Ser
 625 630 635 640
 Lys Thr Glu Lys Arg Leu Ser Asn Val Phe Asp Ile Glu Thr Met Phe
 645 650 655
 Arg Glu Tyr Asn Tyr Tyr Thr Gln Asn Leu Asn Gly Leu Arg Lys Asp
 660 665 670
 Leu Asp Asp Ser Ile Asp His Gly Arg Asp Ser Phe Ile Gln Thr Leu
 675 680 685
 Gly Asp Ile Met Gln Asp Leu Gly Thr Ile Gly Lys Val Val Val Asn
 690 695 700

Val Ala Ser Gly Val Phe Ser Leu Phe Gly Ser Ile Val Ser Gly Val
705 710 715 720

Ile Ser Phe Phe Lys Asn Pro Phe Gly Gly Met Leu Leu Ile Val Leu
725 730 735

Ile Ile Ala Gly Val Val Val Val Tyr Leu Phe Met Thr Arg Ser Arg
740 745 750

Ser Ile Tyr Ser Ala Pro Ile Arg Met Leu Tyr Pro Gly Val Glu Arg
755 760 765

Ala Ala Gln Glu Pro Gly Ala His Pro Val Ser Glu Asp Gln Ile Arg
770 775 780

Asn Ile Leu Met Gly Met His Gln Phe Gln Gln Arg Gln Arg Ala Glu
785 790 795 800

Glu Glu Ala Arg Arg Glu Glu Glu Val Lys Gly Lys Arg Thr Leu Phe
805 810 815

Glu Val Ile Arg Asp Ser Ala Thr
820

<210> 44

<211> 818

<212> PRT

<213> Equine herpesvirus 5

<400> 44

Met Val Ala Trp Phe Gly Leu Trp Gly Phe Ala Arg Leu Met Ala Thr
1 5 10 15

Leu Ala Leu Leu Cys Gly Arg Val Ala Leu Asp Glu Ser Ser Ala Thr
20 25 30

Pro Ser Ile Pro Pro Thr His Lys Pro Ala Val His His Glu Asp Asn
35 40 45

Thr Thr Asn Pro Phe Leu Leu Phe Arg Val Cys Gly Ala Ser Pro Thr
50 55 60

Gly Glu Ile Phe Arg Phe Pro Leu Glu Glu Asn Cys Pro Asn Thr Glu
65 70 75 80

Asp Lys Glu His Val Glu Gly Ile Leu Leu Ile Tyr Lys Thr Asn Ile
85 90 95

Val Pro Tyr Ile Phe Asn Val Arg Lys Tyr Arg Lys Leu Val Thr Ser
100 105 110

Thr Thr Ile Tyr Lys Gly Trp Ser Gln Asp Ala Ile Thr Asn Gln Tyr
115 120 125

Thr Ser Ser Phe Ala Met Pro Leu Trp Glu Ala Arg Leu Val Asp Tyr
130 135 140

Asn	Tyr	Glu	Cys	Tyr	Asn	Gly	Ile	Gln	Val	Thr	Glu	Asn	Gly	His	Leu	145	150	155	160
Thr	Thr	Tyr	Val	Asp	Arg	Asp	Gly	Tyr	Asn	Glu	Ser	Val	Arg	Leu	Val	165	170		175
Pro	Ala	Asp	Gly	Leu	Thr	Ser	Ser	Ile	Arg	Arg	Tyr	His	Ser	Gln	Pro	180	185		190
Glu	Leu	Tyr	Val	Thr	Pro	Arg	Asn	Leu	Leu	Trp	Ser	Tyr	Thr	Thr	Arg	195	200		205
Thr	Thr	Val	Asn	Cys	Glu	Val	Ile	Asp	Met	Thr	Ala	Arg	Ser	His	Lys	210	215		220
Pro	Phe	Glu	Tyr	Phe	Val	Thr	Ala	Ser	Gly	Asp	Ser	Ile	Glu	Thr	Ser	225	230	235	240
Pro	Phe	Tyr	Thr	Asn	Ala	Ser	Arg	Arg	Val	Pro	Val	Gln	Val	Leu	Tyr	245	250		255
Asn	Tyr	Ser	Val	Thr	Asp	Tyr	Gly	Val	Gly	Leu	Gly	Ser	Gly	Glu	Asn	260	265		270
Val	Thr	Arg	Phe	Phe	Ala	Thr	Leu	Asn	Asp	Phe	Ser	Ile	Ser	Trp	Lys	275	280		285
Ala	Ala	Thr	Glu	Asn	Ser	Ser	Tyr	Cys	Pro	Leu	Val	Leu	Trp	Lys	Gly	290	295		300
Phe	Pro	Ser	Ala	Ile	Gln	Thr	Lys	His	Glu	Lys	Ser	Tyr	His	Phe	Ile	305	310	315	320
Ala	Asp	Ala	Val	Thr	Ala	Ser	Phe	Thr	Thr	Pro	Leu	Thr	Asp	Glu	Thr	325	330		335
Ser	Tyr	Phe	Asn	Thr	Thr	Tyr	Gln	Cys	Ala	Trp	Gln	Asp	Ile	Glu	Gly	340	345		350
Glu	Ile	Gln	Lys	Arg	Phe	Asp	Pro	Val	Ser	Lys	Thr	His	Ala	Arg	Asn	355	360		365
Gly	Ser	Val	Gln	Ile	Tyr	Lys	Thr	Ser	Gly	Asn	Leu	Tyr	Val	Val	Trp	370	375		380
Gln	Pro	Leu	Val	Gln	Leu	Asp	Leu	Leu	Ala	Ala	His	Ala	Lys	Thr	Ile	385	390	395	400
Asn	Ser	Thr	Asp	Asn	Ser	Thr	Ser	Pro	Thr	Thr	Ala	Pro	Asn	Thr	Thr	405	410		415
Thr	Ser	Thr	Ser	Ser	Arg	Arg	Lys	Arg	Arg	Asp	Thr	Gly	Asn	Thr	Ala	420	425		430
Thr	Asn	Asn	Ser	Ser	Ser	Asn	Asn	Ser	Ser	Met	Glu	Glu	Asn	Leu	Ala	435	440		445

Thr	Ser	Gln	Val	Gln	Phe	Ala	Tyr	Asp	Gln	Leu	Arg	Lys	Ser	Ile	Asn		
450						455					460						
Arg	Val	Leu	Glu	Gln	Leu	Ser	Arg	Val	Trp	Cys	Gln	Asn	Gln	Tyr	Arg		
465					470					475					480		
Ala	Ser	Leu	Met	Trp	Tyr	Glu	Leu	Ser	Lys	Ile	Asn	Pro	Thr	Ser	Val		
				485					490					495			
Met	Ser	Ala	Ile	Tyr	Gly	Arg	Pro	Val	Ser	Ala	Lys	Leu	Val	Gly	Asp		
			500					505					510				
Val	Val	Gln	Ile	Ser	Asp	Cys	Ile	Thr	Val	Asp	Gln	Glu	Ser	Val	Phe		
		515					520					525					
Val	His	Arg	Asn	Leu	Arg	Val	Pro	Gly	Ser	Lys	Asp	Leu	Cys	Tyr	Thr		
	530					535					540						
Arg	Pro	Val	Val	Gly	Phe	Lys	Phe	Ile	Asn	Gly	Ser	Glu	Leu	Phe	Val		
545					550					555					560		
Gly	Gln	Leu	Gly	Ala	Arg	Asn	Glu	Ile	Leu	Leu	Ser	Thr	Asn	Leu	Val		
				565					570					575			
Glu	Val	Cys	Gln	His	Ser	Cys	Glu	His	Tyr	Phe	Gln	Gly	Gly	Asn	His		
			580					585					590				
Ile	Tyr	Lys	Tyr	Lys	Asn	Tyr	Glu	Tyr	Val	Ser	Thr	Met	Asn	Leu	Thr		
		595					600					605					
Asp	Val	Pro	Thr	Leu	His	Thr	Met	Ile	Thr	Leu	Asn	Leu	Ser	Leu	Val		
	610					615					620						
Glu	Asn	Val	Asp	Phe	Gln	Val	Ile	Gln	Leu	Tyr	Ser	Gln	Lys	Glu	Lys		
625					630					635					640		
Lys	Leu	Ser	Asn	Val	Phe	Asp	Ile	Glu	Thr	Met	Phe	Arg	Glu	Tyr	Asn		
				645					650					655			
Tyr	Tyr	Thr	Gln	Asn	Leu	Lys	Gly	Leu	Arg	Lys	Asp	Leu	Asp	Asp	Ser		
			660					665					670				
Ile	His	Asp	Gly	Arg	Asp	Ser	Phe	Ile	Gln	Phe	Leu	Gly	Asp	Leu	Val		
		675					680					685					
Gln	Asp	Leu	Val	Pro	Val	Gly	Asp	Val	Ile	Val	Asn	Val	Ala	Ser	Gly		
	690					695					700						
Val	Phe	Ser	Leu	Phe	Gly	Ser	Ile	Val	Ser	Gly	Val	Ile	Ser	Phe	Leu		
705					710					715					720		
Lys	Asn	Pro	Leu	Gly	Ala	Ile	Leu	Thr	Ile	Ala	Leu	Ile	Val	Gly	Gly		
				725					730					735			
Ile	Ile	Val	Leu	Tyr	Leu	Phe	Ile	Thr	Arg	Ser	Arg	Thr	Val	Tyr	Gln		
			740					745					750				

Ala Pro Ile Arg Met Leu Tyr Pro Glu Val Asp Arg Ala Pro Gln Gln
755 760 765

Asn Val Gln Pro Ile Pro Glu Asp Gln Val Arg Ser Ile Leu Leu Ala
770 775 780

Met His Gln Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
785 790 795 800

Glu Glu His Thr Gln Arg Arg Ser Ile Phe Asp Thr Ile Arg Glu Ser
805 810 815

Thr Ser

<210> 45

<211> 830

<212> PRT

<213> Alcelaphine herpesvirus

<400> 45

Met Ala His Thr Gly Ser Thr Val Cys Ala Phe Leu Ile Phe Ala Val
1 5 10 15

Leu Lys Asn Val Phe Cys Gln Thr Pro Thr Ser Ser Ser Glu Val Glu
20 25 30

Asp Val Ile Pro Glu Ala Asn Thr Val Ser Asp Asn Ile Ile Arg Gln
35 40 45

Gln Arg Asn Asn Thr Ala Lys Gly Ile His Ser Asp Pro Ser Ala Phe
50 55 60

Pro Phe Arg Val Cys Ser Ala Ser Asn Ile Gly Asp Ile Phe Arg Phe
65 70 75 80

Gln Thr Ser His Ser Cys Pro Asn Thr Lys Asp Lys Glu His Asn Glu
85 90 95

Gly Ile Leu Leu Ile Phe Lys Glu Asn Ile Val Pro Tyr Val Phe Lys
100 105 110

Val Arg Lys Tyr Arg Lys Ile Val Thr Thr Ser Thr Ile Tyr Asn Gly
115 120 125

Ile Tyr Ala Asp Ala Val Thr Asn Gln His Val Phe Ser Lys Ser Val
130 135 140

Pro Ile Tyr Glu Thr Arg Arg Met Asp Thr Ile Tyr Gln Cys Tyr Asn
145 150 155 160

Ser Leu Asp Val Thr Val Gly Gly Asn Leu Leu Val Tyr Thr Asp Asn
165 170 175

Asp Gly Ser Asn Met Thr Val Asp Leu Gln Pro Val Asp Gly Leu Ser
180 185 190

Asn Ser Val Arg Arg Tyr His Ser Gln Pro Glu Ile His Ala Glu Pro
 195 200 205
 Gly Trp Leu Leu Gly Gly Tyr Arg Arg Arg Thr Thr Val Asn Cys Glu
 210 215 220
 Val Thr Glu Thr Asp Ala Arg Ala Val Pro Pro Phe Arg Tyr Phe Ile
 225 230 235 240
 Thr Asn Ile Gly Asp Thr Ile Glu Met Ser Pro Phe Trp Ser Lys Ala
 245 250 255
 Trp Asn Glu Thr Glu Phe Ser Gly Glu Pro Asp Arg Thr Leu Thr Val
 260 265 270
 Ala Lys Asp Tyr Arg Val Val Asp Tyr Lys Phe Arg Gly Thr Gln Pro
 275 280 285
 Gln Gly His Thr Arg Ile Phe Val Asp Lys Glu Glu Tyr Thr Leu Ser
 290 295 300
 Trp Ala Gln Gln Phe Arg Asn Ile Ser Tyr Cys Arg Trp Ala His Trp
 305 310 315 320
 Lys Ser Phe Asp Asn Ala Ile Lys Thr Glu His Gly Lys Ser Leu His
 325 330 335
 Phe Val Ala Asn Asp Ile Thr Ala Ser Phe Tyr Thr Pro Asn Thr Gln
 340 345 350
 Thr Arg Glu Val Leu Gly Lys His Val Cys Leu Asn Asn Thr Ile Glu
 355 360 365
 Ser Glu Leu Lys Ser Arg Leu Ala Lys Val Asn Asp Thr His Ser Pro
 370 375 380
 Asn Gly Thr Ala Gln Tyr Tyr Leu Thr Asn Gly Gly Leu Leu Leu Val
 385 390 395 400
 Trp Gln Pro Leu Val Gln Gln Lys Leu Leu Asp Ala Lys Gly Leu Leu
 405 410 415
 Asp Ala Val Lys Lys Gln Gln Asn Thr Thr Thr Thr Thr Thr Thr
 420 425 430
 Arg Ser Arg Arg Gln Arg Arg Ser Val Ser Ser Gly Ile Asp Asp Val
 435 440 445
 Tyr Thr Ala Glu Ser Thr Ile Leu Leu Thr Gln Ile Gln Phe Ala Tyr
 450 455 460
 Asp Thr Leu Arg Ala Gln Ile Asn Asn Val Leu Glu Glu Leu Ser Arg
 465 470 475 480
 Ala Trp Cys Arg Glu Gln His Arg Ala Ser Leu Met Trp Asn Glu Leu
 485 490 495

Ser	Lys	Ile	Asn	Pro	Thr	Ser	Val	Met	Ser	Ser	Ile	Tyr	Gly	Arg	Pro		
			500					505					510				
Val	Ser	Ala	Lys	Arg	Ile	Gly	Asp	Val	Ile	Ser	Val	Ser	His	Cys	Val		
		515					520					525					
Val	Val	Asp	Gln	Asp	Ser	Val	Ser	Leu	His	Arg	Ser	Met	Arg	Val	Pro		
	530					535					540						
Gly	Arg	Asp	Lys	Thr	His	Glu	Cys	Tyr	Ser	Arg	Pro	Pro	Val	Thr	Phe		
545					550					555					560		
Lys	Phe	Ile	Asn	Asp	Ser	His	Leu	Tyr	Lys	Gly	Gln	Leu	Gly	Val	Asn		
			565					570						575			
Asn	Glu	Ile	Leu	Leu	Thr	Thr	Thr	Ala	Val	Glu	Ile	Cys	His	Glu	Asn		
		580						585					590				
Thr	Glu	His	Tyr	Phe	Gln	Gly	Gly	Asn	Asn	Met	Tyr	Phe	Tyr	Lys	Asn		
	595					600						605					
Tyr	Arg	His	Val	Lys	Thr	Met	Pro	Val	Gly	Asp	Val	Ala	Thr	Leu	Asp		
	610					615					620						
Thr	Phe	Met	Val	Leu	Asn	Leu	Thr	Leu	Val	Glu	Asn	Ile	Asp	Phe	Gln		
625					630					635					640		
Val	Ile	Glu	Leu	Tyr	Ser	Arg	Glu	Glu	Lys	Arg	Met	Ser	Thr	Ala	Phe		
			645						650					655			
Asp	Ile	Glu	Thr	Met	Phe	Arg	Glu	Tyr	Asn	Tyr	Tyr	Thr	Gln	Arg	Val		
		660						665					670				
Thr	Gly	Leu	Arg	Arg	Asp	Leu	Thr	Asp	Leu	Ala	Thr	Asn	Arg	Asn	Gln		
	675					680						685					
Phe	Val	Asp	Ala	Phe	Gly	Ser	Leu	Met	Asp	Asp	Leu	Gly	Val	Val	Gly		
	690					695					700						
Lys	Thr	Val	Leu	Asn	Ala	Val	Ser	Ser	Val	Ala	Thr	Leu	Phe	Ser	Ser		
705				710						715					720		
Ile	Val	Ser	Gly	Ile	Ile	Asn	Phe	Ile	Lys	Asn	Pro	Phe	Gly	Gly	Met		
			725					730						735			
Leu	Leu	Phe	Gly	Leu	Ile	Ala	Ala	Val	Val	Ile	Thr	Val	Ile	Leu	Leu		
		740						745					750				
Asn	Arg	Lys	Ala	Lys	Arg	Phe	Ala	Gln	Asn	Pro	Val	Gln	Met	Ile	Tyr		
	755					760						765					
Pro	Asp	Ile	Lys	Thr	Ile	Thr	Ser	Gln	Arg	Glu	Glu	Leu	Gln	Val	Asp		
	770				775						780						
Pro	Ile	Ser	Lys	His	Glu	Leu	Asp	Arg	Ile	Met	Leu	Ala	Met	His	Asp		
785				790						795					800		

Tyr His Ala Ser Lys Gln Pro Glu Ser Lys Gln Asp Glu Glu Gln Gly
805 810 815

Ser Thr Thr Ser Gly Pro Ala Asp Trp Leu Asn Lys Ala Lys
820 825 830

<210> 46

<211> 829

<212> PRT

<213> Epstein-Barr virus

<400> 46

Met Thr Arg Arg Arg Val Leu Ser Val Val Val Leu Leu Ala Ala Leu
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Ala Cys Arg Leu Gly Ala Gln Thr Pro Glu Gln Pro Ala Pro Pro Ala
20 25 30

Thr Thr Val Gln Pro Thr Ala Thr Arg Gln Gln Thr Ser Phe Pro Phe
35 40 45

Arg Val Cys Glu Leu Ser Ser His Gly Asp Leu Phe Arg Phe Ser Ser
50 55 60

Asp Ile Gln Cys Pro Ser Phe Gly Thr Arg Glu Asn His Thr Glu Gly
65 70 75 80

Leu Leu Met Val Phe Lys Asp Asn Ile Ile Pro Tyr Ser Phe Lys Val
85 90 95

Arg Ser Tyr Thr Lys Ile Val Thr Asn Ile Leu Ile Tyr Asn Gly Trp
100 105 110

Tyr Ala Asp Ser Val Thr Asn Arg His Glu Glu Lys Phe Ser Val Asp
115 120 125

Ser Tyr Glu Thr Asp Gln Met Asp Thr Ile Tyr Gln Cys Tyr Asn Ala
130 135 140

Val Lys Met Thr Lys Asp Gly Leu Thr Arg Val Tyr Val Asp Arg Asp
145 150 155 160

Gly Val Asn Ile Thr Val Asn Leu Lys Pro Thr Gly Gly Leu Ala Asn
165 170 175

Gly Val Arg Arg Tyr Ala Ser Gln Thr Glu Leu Tyr Asp Ala Pro Gly
180 185 190

Trp Leu Ile Trp Thr Tyr Arg Thr Arg Thr Thr Val Asn Cys Leu Ile
195 200 205

Thr Asp Met Met Ala Lys Ser Asn Ser Pro Phe Asp Phe Phe Val Thr
210 215 220

Thr Thr Gly Gln Thr Val Glu Met Ser Pro Phe Tyr Asp Gly Lys Asn
225 230 235 240

Lys	Glu	Thr	Phe	His	Glu	Arg	Ala	Asp	Ser	Phe	His	Val	Arg	Thr	Asn	
				245					250						255	
Tyr	Lys	Ile	Val	Asp	Tyr	Asp	Asn	Arg	Gly	Thr	Asn	Pro	Gln	Gly	Glu	
			260					265					270			
Arg	Arg	Ala	Phe	Leu	Asp	Lys	Gly	Thr	Tyr	Thr	Leu	Ser	Trp	Lys	Leu	
		275					280					285				
Glu	Asn	Arg	Thr	Ala	Tyr	Cys	Pro	Leu	Gln	His	Trp	Gln	Thr	Phe	Asp	
	290					295					300					
Ser	Thr	Ile	Ala	Thr	Glu	Thr	Gly	Lys	Ser	Ile	His	Phe	Val	Thr	Asp	
305					310					315					320	
Glu	Gly	Thr	Ser	Ser	Phe	Val	Thr	Asn	Thr	Thr	Val	Gly	Ile	Glu	Leu	
			325					330					335			
Pro	Asp	Ala	Phe	Lys	Cys	Ile	Glu	Glu	Gln	Val	Asn	Lys	Thr	Met	His	
		340						345					350			
Glu	Lys	Tyr	Glu	Ala	Val	Gln	Asp	Arg	Tyr	Thr	Lys	Gly	Gln	Glu	Ala	
		355					360					365				
Ile	Thr	Tyr	Phe	Ile	Thr	Ser	Gly	Gly	Leu	Leu	Leu	Ala	Trp	Leu	Pro	
	370					375					380					
Leu	Thr	Pro	Arg	Ser	Leu	Ala	Thr	Val	Lys	Asn	Leu	Thr	Glu	Leu	Thr	
385					390					395					400	
Thr	Pro	Thr	Ser	Ser	Pro	Pro	Ser	Ser	Pro	Ser	Pro	Pro	Ala	Pro	Ser	
			405					410						415		
Ala	Ala	Arg	Gly	Ser	Thr	Pro	Ala	Ala	Val	Leu	Arg	Arg	Arg	Arg	Arg	
		420						425				430				
Asp	Ala	Gly	Asn	Ala	Thr	Thr	Pro	Val	Pro	Pro	Thr	Ala	Pro	Gly	Lys	
	435						440					445				
Ser	Leu	Gly	Thr	Leu	Asn	Asn	Pro	Ala	Thr	Val	Gln	Ile	Gln	Phe	Ala	
	450				455						460					
Tyr	Asp	Ser	Leu	Arg	Arg	Gln	Ile	Asn	Arg	Met	Leu	Gly	Asp	Leu	Ala	
465					470				475						480	
Arg	Ala	Trp	Cys	Leu	Glu	Gln	Lys	Arg	Gln	Asn	Met	Val	Leu	Arg	Glu	
			485					490					495			
Leu	Thr	Lys	Ile	Asn	Pro	Thr	Thr	Val	Met	Ser	Ser	Ile	Tyr	Gly	Lys	
		500						505					510			
Ala	Val	Ala	Ala	Lys	Arg	Leu	Gly	Asp	Val	Ile	Ser	Val	Ser	Gln	Cys	
		515					520					525				
Val	Pro	Val	Asn	Gln	Ala	Thr	Val	Thr	Leu	Arg	Lys	Ser	Met	Arg	Val	
	530					535					540					

Pro Gly Ser Glu Thr Met Cys Tyr Ser Arg Pro Leu Val Ser Phe Ser
 545 550 555 560
 Phe Ile Asn Asp Thr Lys Thr Tyr Glu Gly Gln Leu Gly Thr Asp Asn
 565 570 575
 Glu Ile Phe Leu Thr Lys Lys Met Thr Glu Val Cys Gln Ala Thr Ser
 580 585 590
 Gln Tyr Tyr Phe Gln Ser Gly Asn Glu Ile His Val Tyr Asn Asp Tyr
 595 600 605
 His His Phe Lys Thr Ile Glu Leu Asp Gly Ile Ala Thr Leu Gln Thr
 610 615 620
 Phe Ile Ser Leu Asn Thr Ser Leu Ile Glu Asn Ile Asp Phe Ala Ser
 625 630 635 640
 Leu Glu Leu Tyr Ser Arg Asp Glu Gln Arg Ala Ser Asn Val Phe Asp
 645 650 655
 Leu Glu Gly Ile Phe Arg Glu Tyr Asn Phe Gln Ala Gln Asn Ile Ala
 660 665 670
 Gly Leu Arg Lys Asp Leu Asp Asn Ala Val Ser Asn Gly Arg Asn Gln
 675 680 685
 Phe Val Asp Gly Leu Gly Glu Leu Met Asp Ser Leu Gly Ser Val Gly
 690 695 700
 Gln Ser Ile Thr Asn Leu Val Ser Thr Val Gly Gly Leu Phe Ser Ser
 705 710 715 720
 Leu Val Ser Gly Phe Ile Ser Phe Phe Lys Asn Pro Phe Gly Gly Met
 725 730 735
 Leu Ile Leu Val Leu Val Ala Gly Val Val Ile Leu Val Ile Ser Leu
 740 745 750
 Thr Arg Arg Thr Arg Gln Met Ser Gln Gln Pro Val Gln Met Leu Tyr
 755 760 765
 Pro Gly Ile Asp Glu Leu Ala Gln Gln His Ala Ser Gly Glu Gly Pro
 770 775 780
 Gly Ile Asn Pro Ile Ser Lys Thr Glu Leu Gln Ala Ile Met Leu Ala
 785 790 795 800
 Leu His Glu Gln Asn Gln Glu Gln Lys Arg Ala Ala Gln Arg Ala Ala
 805 810 815
 Gly Pro Ser Val Ala Ser Arg Ala Leu Gln Ala Ala Arg
 820 825

<210> 47
 <211> 660
 <212> DNA

<213> artificial

<220>

<223> Suid herpesvirus 1 - bases 641-1300

<400> 47

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cgccgcccgtc cggtccacg gtggtgcggc tggagcccga gcaggcctgc cccgagtact      60
cgcaggggcg caacttcacg gaggggatcg ccgtgctctt caaggagaac atcgccccgc      120
acaagttcaa ggccacatc tactacaaga acgtcatcgt cacgaccgtg tgggccggga      180
gcacgtacgc ggccatcacg aaccgcttca cagaccgctg gcccgtcccc gtgcaggaga      240
tcacggacgt gatcgaccgc cgcggcaagt gcgtctccaa ggccgagtag gtgcgcaaca      300
accacaaggt gaccgccttc gaccgcgacg agaaccccggt cgaggtggac ctgcgcccct      360
cgcgcctgaa cgcgctcggc acccgcggtt ggcacaccac caacgacacc tacaccaaga      420
tcggcgccgc gggctttctac cacacgggca cctccgtcaa ctgcatcgtc gaggaggtgg      480
aggcgcgctc cgtgtacccc tacgactcct tcgccctgtc cacgggggac attgtgtaca      540
tgtccccctt ctacggcctg cgcgaggggg cccacgggga gcacatcggc tacgcgcccg      600
ggcgcttcca gcaggtggag cactactacc ccatcgacct ggactcgcgc ctccgcgcct      660
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<210> 48

<211> 359

<212> PRT

<213> artificial

<220>

<223> Suid herpesvirus 1 - bases 491-850

<400> 48

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Ala Ala Pro Ala Ala Ala Arg Arg Ala Arg Arg Ser Pro Gly Pro Ala
1          5          10          15

Gly Thr Pro Glu Pro Pro Ala Val Asn Gly Thr Gly His Leu Arg Ile
          20          25          30

Thr Thr Gly Ser Ala Glu Phe Ala Arg Leu Gln Phe Thr Tyr Asp His
          35          40          45

Ile Gln Ala His Val Asn Asp Met Leu Gly Arg Ile Ala Ala Ala Trp
50          55          60

Cys Glu Leu Gln Asn Lys Asp Arg Thr Leu Trp Ser Glu Met Ser Arg
65          70          75          80

Leu Asn Pro Ser Ala Val Ala Thr Ala Ala Leu Gly Gln Arg Val Ser
          85          90          95

Ala Arg Met Leu Gly Asp Val Met Ala Ile Ser Arg Cys Val Glu Val
100         105         110

Arg Gly Gly Val Tyr Val Gln Asn Ser Met Arg Val Pro Gly Glu Arg
115         120         125

Gly Thr Cys Tyr Ser Arg Pro Leu Val Thr Phe Glu His Asn Gly Thr
130         135         140

Gly Val Ile Glu Gly Gln Leu Gly Asp Asp Asn Glu Leu Leu Ile Ser
145         150         155         160
```

Arg Asp Leu Ile Glu Pro Cys Thr Gly Asn His Arg Arg Tyr Phe Lys
 165 170 175
 Leu Gly Ser Gly Tyr Val Tyr Tyr Glu Asp Tyr Asn Tyr Val Arg Met
 180 185 190
 Val Glu Val Pro Glu Thr Ile Ser Thr Arg Val Thr Leu Asn Leu Thr
 195 200 205
 Leu Leu Glu Asp Arg Glu Phe Leu Pro Leu Glu Val Tyr Thr Arg Glu
 210 215 220
 Glu Leu Ala Asp Thr Gly Leu Leu Asp Tyr Ser Glu Ile Gln Arg Arg
 225 230 235 240
 Asn Gln Leu His Ala Leu Lys Phe Tyr Asp Ile Asp Arg Val Val Lys
 245 250 255
 Val Asp His Asn Val Val Leu Leu Arg Gly Ile Ala Asn Phe Phe Gln
 260 265 270
 Gly Leu Gly Asp Val Gly Ala Ala Val Gly Lys Val Val Leu Gly Ala
 275 280 285
 Thr Gly Ala Val Ile Ser Ala Val Gly Gly Met Val Ser Phe Leu Ser
 290 295 300
 Asn Pro Phe Gly Ala Leu Ala Ile Gly Leu Leu Val Leu Ala Gly Leu
 305 310 315 320
 Val Ala Ala Phe Leu Ala Tyr Arg His Ile Ser Arg Leu Arg Arg Asn
 325 330 335
 Pro Met Lys Ala Leu Tyr Pro Val Thr Thr Lys Thr Leu Lys Glu Asp
 340 345 350
 Gly Val Asp Glu Gly Asp Val
 355

<210> 49
 <211> 420
 <212> DNA
 <213> Suid herpesvirus 2

<400> 49
 ccagcataat gatagccaat aatctgtgtt actctaccct gatcttaaat gacgaggacg 60
 tgacggggat cgacgagaaa gatattctga cgggtgcatgt aaacaagaat accgtgtaca 120
 gggttcgttag gacgagcgtc agggagtcta tactcggcac gctgctgtct agatggctca 180
 ggaagagaaa ggaagtgaag gcgcgcatga aacgctgtga ggaccctatg ttggcactga 240
 tacttgacaa gcagcagctt gccctcaagg tgacgtgcaa tgcgttttac ggcttcacgg 300
 gagcgtgca cggctctgctg ccgtgtctcc ctctagcggc gtccatcacc agcatagggc 360
 gggacatgct taggcagacg agtgacttta tcaacaatgt cctttcgtct agagaatacg 420

<210> 50
 <211> 159

<212> PRT

<213> Suid herpesvirus 2

<400> 50

Ser Ile Met Ile Ala Asn Asn Leu Cys Tyr Ser Thr Leu Ile Leu Asn
1 5 10 15

Asp Glu Asp Val Thr Gly Ile Asp Glu Lys Asp Ile Leu Thr Val His
20 25 30

Val Asn Lys Asn Thr Val Tyr Arg Phe Val Arg Ser Ser Val Arg Glu
35 40 45

Ser Ile Leu Gly Thr Leu Leu Ser Arg Trp Leu Arg Lys Arg Lys Glu
50 55 60

Val Lys Ala Arg Met Lys Arg Cys Glu Asp Pro Met Leu Ala Leu Ile
65 70 75 80

Leu Asp Lys Gln Gln Leu Ala Leu Lys Val Thr Cys Asn Ala Phe Tyr
85 90 95

Gly Phe Thr Gly Ala Val His Gly Leu Leu Pro Cys Leu Pro Leu Ala
100 105 110

Ala Ser Ile Thr Ser Ile Gly Arg Asp Met Leu Arg Gln Thr Ser Asp
115 120 125

Phe Ile Asn Asn Val Leu Ser Ser Arg Glu Tyr Val Ser Glu Lys Phe
130 135 140

Ser Leu Ser Asp Gly Asp Phe Gln Gly Asp Phe Ser Pro Glu Cys
145 150 155

<210> 51

<211> 466

<212> DNA

<213> artificial

<220>

<223> Portion of porcine gamma herpesvirus polymerase - AF118399

<400> 51

taatctatgt	cactctaccc	taatccatca	tgaagacctg	cataaatatc	ctcaattaaa	60
ggaggaggat	tatgaaacat	ttttgattag	ttctggtcct	gttcactttg	taaaaaaaca	120
catatcagaa	tctcttctgt	ctaacctgct	tacaacatgg	ctggctaaga	gaaaaatgat	180
cagaaaggaa	ttagcagcat	gtgctgacct	aaagctcagg	acaatttttag	ataaacagca	240
gcttgcaatt	aaggtgacat	gcaatgctgt	gtatgggttc	actggtgttg	catctggtat	300
gctgcctgt	ctcaagattg	cagagacct	aactatgcaa	ggaaggcca	tgttggaata	360
gacaaaagta	ttttagaga	atttaagtca	tgaggatctc	cattccatct	gtaagggttg	420
ctttatgcct	cagtcaccaa	acagcattga	taaacccttc	aagggtg		466

<210> 52

<211> 423

<212> DNA

<213> artificial

<220>

<223> Portion of porcine gamma herpesvirus polymerase - AF118401

<400> 52

gaggacctgc	ataagtatcc	tcaattaaag	gaggatgatt	atgaaacatt	tttgattagt	60
tctggccctg	ttcactttgt	aaaaaaacac	atatacagaat	ctcttctgtc	gaacttgctc	120
acaacatggc	tgccaagag	aaaaatgatc	agaaaggaat	tgacagcatg	tgctgatcca	180
aagctcagga	caattttaga	taaacagcag	cttgcaatta	aggtgacatg	caatgctgtg	240
tatggattca	ctgggtgttc	atctgggtatg	ctgccatgtc	tcaagattgc	agagaccatc	300
actatgcaag	gaagggccat	gttggaagaa	acaaaagtat	ttgtagagaa	tctgagtcac	360
gaagatctcc	gttccatgat	taaggttggc	tctataacctc	agtcacataa	cgtgtttgat	420
aaa						423

<210> 53

<211> 292

<212> DNA

<213> artificial

<220>

<223> Portion of Acelaphine herpesvirus.

<400> 53

aagtaataga	actatactct	agagaagaga	agaggatgag	cactgcattt	gatatagaga	60
ccatgttttag	agaatacaac	tactacacac	agaggggtcac	tgccctgcgg	agggacttga	120
cagacctagc	tacaaacaga	aatcaatttg	tagatgcctt	tgccagcctc	atggacgact	180
tgggggtcgt	ggggaaaacg	gtgttgaaatg	ctgtgagcag	tgtggccaca	ctcttcagct	240
ctatagtctc	agggatcatc	aatttcatta	aaaaccctt	tgggggaatg	tt	292

<210> 54

<211> 152

<212> DNA

<213> artificial

<220>

<223> Portion of Acelaphine herpesvirus.

<400> 54

tggtgccgtg	agcagcaccg	agcctctctc	atgtggaacg	agctaagcaa	aatcaaccct	60
accagtgtga	tgagctctat	atacggggcg	ccagtatctg	ccaaaagaat	tggagatgtg	120
atatctgtct	ctcactgtgt	ggtggtggac	ca			152

<210> 55

<211> 793

<212> PRT

<213> artificial

<220>

<223> Portion of Acelaphine herpesvirus.

<400> 55

Lys	Gly	Ile	His	Ser	Asp	Pro	Ser	Ala	Phe	Pro	Phe	Arg	Val	Cys	Ser
1				5					10					15	

Ala Ser Asn Ile Gly Asp Ile Phe Arg Phe Gln Thr Ser His Ser Cys
 20 25 30
 Pro Asn Thr Lys Asp Lys Glu His Asn Glu Gly Ile Leu Leu Ile Phe
 35 40 45
 Lys Glu Asn Ile Val Pro Tyr Val Phe Lys Val Arg Lys Tyr Arg Lys
 50 55 60
 Ile Val Thr Thr Ser Thr Ile Tyr Asn Gly Ile Tyr Ala Asp Ala Val
 65 70 75 80
 Thr Asn Gln His Val Phe Ser Lys Ser Val Pro Ile Tyr Glu Thr Arg
 85 90 95
 Arg Met Asp Thr Ile Tyr Gln Cys Tyr Asn Ser Leu Asp Val Thr Val
 100 105 110
 Gly Gly Asn Leu Leu Val Tyr Thr Asp Asn Asp Gly Ser Asn Met Thr
 115 120 125
 Val Asp Leu Gln Pro Val Asp Gly Leu Ser Asn Ser Val Arg Arg Tyr
 130 135 140
 His Ser Gln Pro Glu Ile His Ala Glu Pro Gly Trp Leu Leu Gly Gly
 145 150 155 160
 Tyr Arg Arg Arg Thr Thr Val Asn Cys Glu Val Thr Glu Thr Asp Ala
 165 170 175
 Arg Ala Val Pro Pro Phe Arg Tyr Phe Ile Thr Asn Ile Gly Asp Thr
 180 185 190
 Ile Glu Met Ser Pro Phe Trp Ser Lys Ala Trp Asn Glu Thr Glu Phe
 195 200 205
 Ser Gly Glu Pro Asp Arg Thr Leu Thr Val Ala Lys Asp Tyr Arg Val
 210 215 220
 Val Asp Tyr Lys Phe Arg Gly Thr Gln Pro Gln Gly His Thr Arg Ile
 225 230 235 240
 Phe Val Asp Lys Glu Glu Tyr Thr Leu Ser Trp Ala Gln Gln Phe Arg
 245 250 255
 Asn Ile Ser Tyr Cys Arg Trp Ala His Trp Lys Ser Phe Asp Asn Ala
 260 265 270
 Ile Lys Thr Glu His Gly Lys Ser Leu His Phe Val Ala Asn Asp Ile
 275 280 285
 Thr Ala Ser Phe Tyr Thr Pro Asn Thr Gln Thr Arg Glu Val Leu Gly
 290 295 300
 Lys His Val Cys Leu Asn Asn Thr Ile Glu Ser Glu Leu Lys Ser Arg
 305 310 315 320

Leu Ala Lys Val Asn Asp Thr His Ser Pro Asn Gly Thr Ala Gln Tyr
 325 330 335
 Tyr Leu Thr Asn Gly Gly Leu Leu Leu Val Trp Gln Pro Leu Val Gln
 340 345 350
 Gln Lys Leu Leu Asp Ala Lys Gly Leu Leu Asp Ala Val Lys Lys Gln
 355 360 365
 Gln Asn Thr Thr Thr Thr Thr Thr Thr Thr Arg Ser Arg Arg Gln Arg
 370 375 380
 Arg Ser Val Ser Ser Gly Ile Asp Asp Val Tyr Thr Ala Glu Ser Thr
 385 390 395 400
 Ile Leu Leu Thr Gln Ile Gln Phe Ala Tyr Asp Thr Leu Arg Ala Gln
 405 410 415
 Ile Asn Asn Val Leu Glu Glu Leu Ser Arg Ala Trp Cys Arg Glu Gln
 420 425 430
 His Arg Ala Ser Leu Met Trp Asn Glu Leu Ser Lys Ile Asn Pro Thr
 435 440 445
 Ser Val Met Ser Ser Ile Tyr Gly Arg Pro Val Ser Ala Lys Arg Ile
 450 455 460
 Gly Asp Val Ile Ser Val Ser His Cys Val Val Val Asp Gln Asp Ser
 465 470 475 480
 Val Ser Leu His Arg Ser Met Arg Val Pro Gly Arg Asp Lys Thr His
 485 490 495
 Glu Cys Tyr Ser Arg Pro Pro Val Thr Phe Lys Phe Ile Asn Asp Ser
 500 505 510
 His Leu Tyr Lys Gly Gln Leu Gly Val Asn Asn Glu Ile Leu Leu Thr
 515 520 525
 Thr Thr Ala Val Glu Ile Cys His Glu Asn Thr Glu His Tyr Phe Gln
 530 535 540
 Gly Gly Asn Asn Met Tyr Phe Tyr Lys Asn Tyr Arg His Val Lys Thr
 545 550 555 560
 Met Pro Val Gly Asp Val Ala Thr Leu Asp Thr Phe Met Val Leu Asn
 565 570 575
 Leu Thr Leu Val Glu Asn Ile Asp Phe Gln Val Ile Glu Leu Tyr Ser
 580 585 590
 Arg Glu Glu Lys Arg Met Ser Thr Ala Phe Asp Ile Glu Thr Met Phe
 595 600 605
 Arg Glu Tyr Asn Tyr Tyr Thr Gln Arg Val Thr Gly Leu Arg Arg Asp
 610 615 620

Leu Thr Asp Leu Ala Thr Asn Arg Asn Gln Phe Val Asp Ala Phe Gly
 625 630 635 640
 Ser Leu Met Asp Asp Leu Gly Val Val Gly Lys Thr Val Leu Asn Ala
 645 650 655
 Val Ser Ser Val Ala Thr Leu Phe Ser Ser Ile Val Ser Gly Ile Ile
 660 665 670
 Asn Phe Ile Lys Asn Pro Phe Gly Gly Met Leu Leu Phe Gly Leu Ile
 675 680 685
 Ala Ala Val Val Ile Thr Val Ile Leu Leu Asn Arg Lys Ala Lys Arg
 690 695 700
 Phe Ala Gln Asn Pro Val Gln Met Ile Pro Asp Ile Lys Thr Ile Thr
 705 710 715 720
 Ser Gln Arg Glu Glu Leu Gln Val Asp Pro Ile Ser Lys His Glu Leu
 725 730 735
 Asp Arg Ile Met Leu Ala Met His Asp Tyr His Ala Ser Lys Gln Pro
 740 745 750
 Glu Ser Lys Gln Asp Glu Glu Gln Gly Ser Thr Thr Ser Gly Pro Ala
 755 760 765
 Asp Leu Asn Lys Ala Lys Asn Val Leu Arg Arg Arg Ala Gly Tyr Lys
 770 775 780
 Pro Leu Lys Arg Thr Asp Ser Phe Glu
 785 790